

# Process Rate Semantics

Representing Biochemical Systems as  
Collectives of Interacting Automata

Luca Cardelli

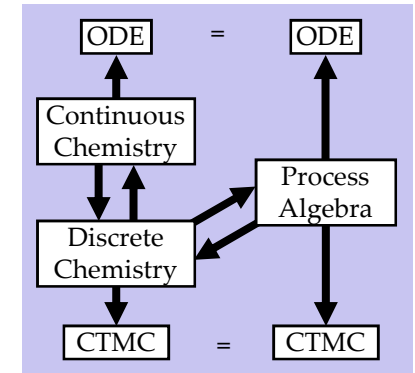
Microsoft Research

Computational and Systems Biology Course  
CoSBI, Trento, 2008-03-13

<http://LucaCardelli.name>

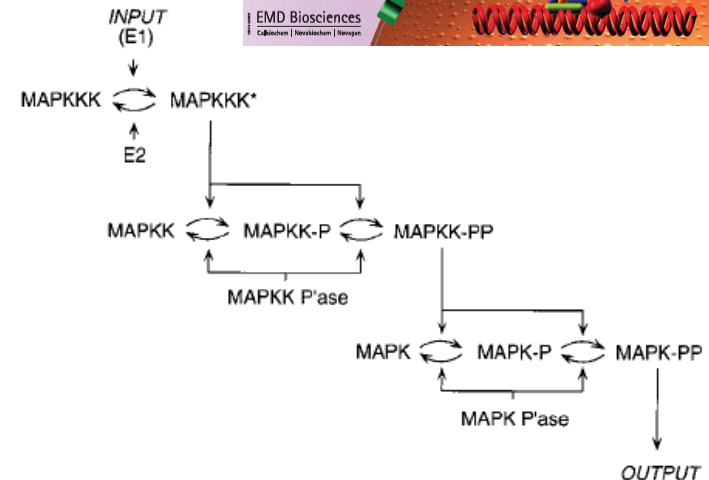
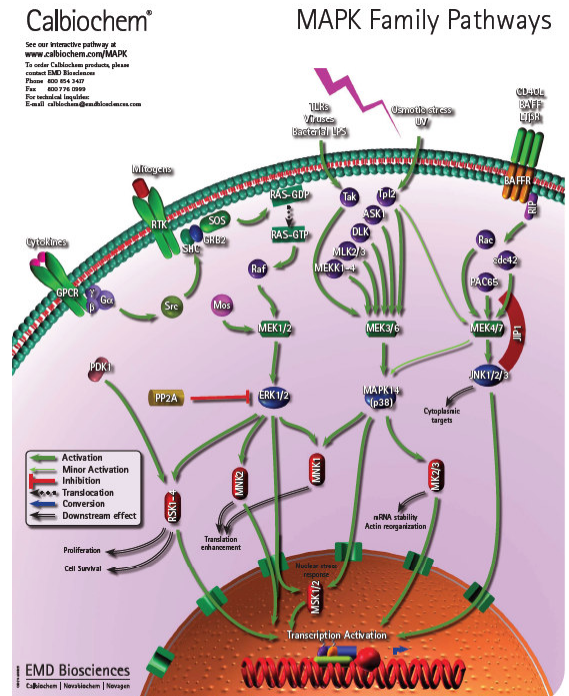
# Aims

- **Connections between modeling approaches**
  - Connecting the **discrete/concurrent/stochastic/molecular** approach
  - to the **continuous/sequential/deterministic/population** approach
- **Connecting syntax with semantics**
  - **Syntax** = model (equations/programs/diagrams/blobs etc.)
  - **Semantics** = state space (generated by the syntax)
  - N.B. model  $\neq$  state space !!
    - The same model can be interpreted in different state spaces
    - Different models can have the same state space
    - Different models of the same state space can support different analysis
- **Ultimately, connections between analysis techniques**
  - We need (and sometimes have) good semantic techniques to analyze state spaces (e.g. calculus, but also modelchecking)
  - But we need equally good syntactic techniques to structure complex models (e.g. compositionality) and analyze them (e.g. process algebra)



# Motivation: Cells Compute

- No survival without computation!
  - Finding food
  - Avoiding predators
- How do they compute?
  - Unusual computational paradigms.
  - Proteins: do they work like electronic circuits?
  - Genes: what kind of software is that?
- Signaling networks
  - Clearly "information processing"
  - They are "just chemistry": molecule interactions
  - But what are their principles and algorithms?
- Complex, higher-order interactions
  - MAPKKK = MAP Kinase Kinase Kinase: that which operates on that which operates on that which operates on protein.
- General models of biological computation
  - What are the appropriate ones?



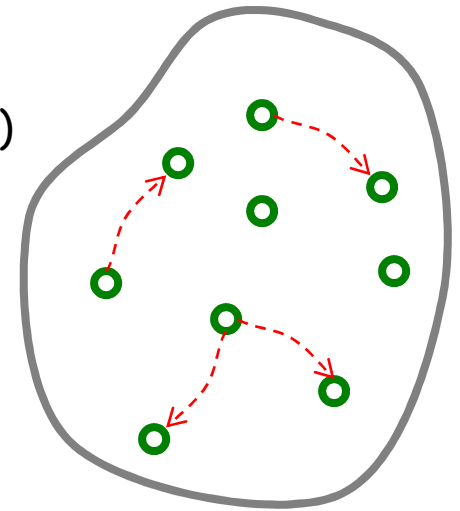
**Ultrasensitivity in the mitogen-activated protein cascade,**  
 Chi-Ying F. Huang and James E. Ferrell, Jr., 1996, *Proc. Natl. Acad. Sci. USA*, 93, 10078-10083.

# (Macro)Molecules as Interacting Automata

- Concurrent (math is based on processes, not functions)
  - Asynchronous (no global clock)
  - Stochastic (or nondeterministic)
  - Stateful (e.g. phosphorylation state)
  - Discrete (transitions between states)
  - Interacting (an "interaction" can be pretty much anything you want that changes molecular state)
- 
- Based on work on process algebra and biological modeling; see references in related papers.

# Stochastic Automata Collectives

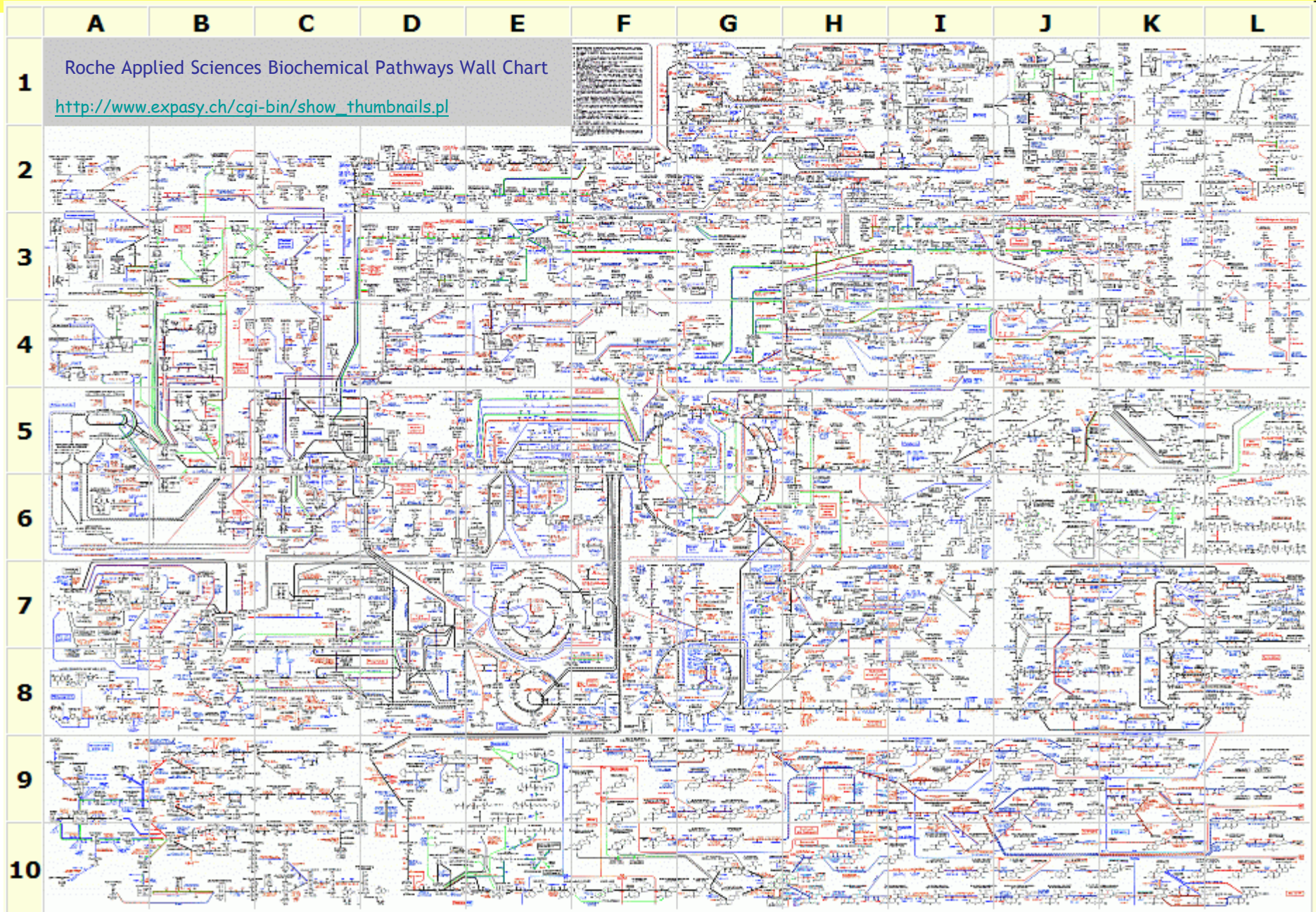
- "Collective":
  - A large set of interacting finite state automata:
    - Not quite language automata ("large set")
    - Not quite cellular automata ("interacting" but not on a grid)
    - Not quite process algebra ("collective behavior")
    - Cf. multi-agent systems and swarm intelligence
- "Stochastic":
  - Interactions have *rates*
    - Not quite discrete (hundreds or thousands of components)
    - Not quite continuous (non-trivial stochastic effects)
    - Not quite hybrid (no "switching" between regimes)
- Very much like biochemistry
  - Which is a large set of stochastically interacting molecules/proteins
  - Are proteins **finite state** and subject to automata-like **transitions**?
    - Let's say they are, at least because:
    - Much of the knowledge being accumulated in Systems Biology is described as state transition diagrams [Kitano].





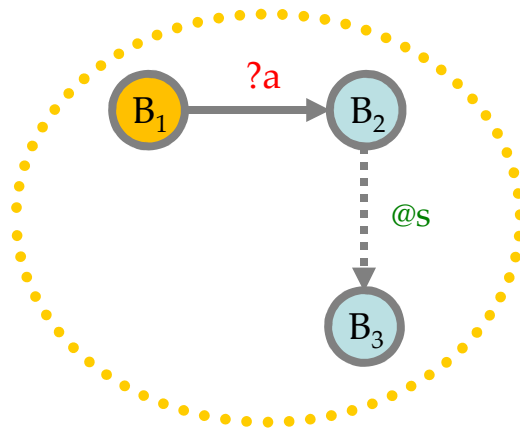
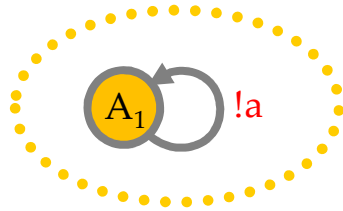


# Compositionality (NOT!)



# Interacting Automata

- Current State
- ⋯→ Decay
- Transition
- ⋯▶ Interaction



$A_1$  is a *state*

$a$  is a *channel* i.e. a named *interaction interface* (e.g. a surface patch)

$?a, !a$  indicate any *complementarity* of interaction (e.g. charge)

$?a, !a$  indicate *complementary actions*,

$@r, @s$  are rates

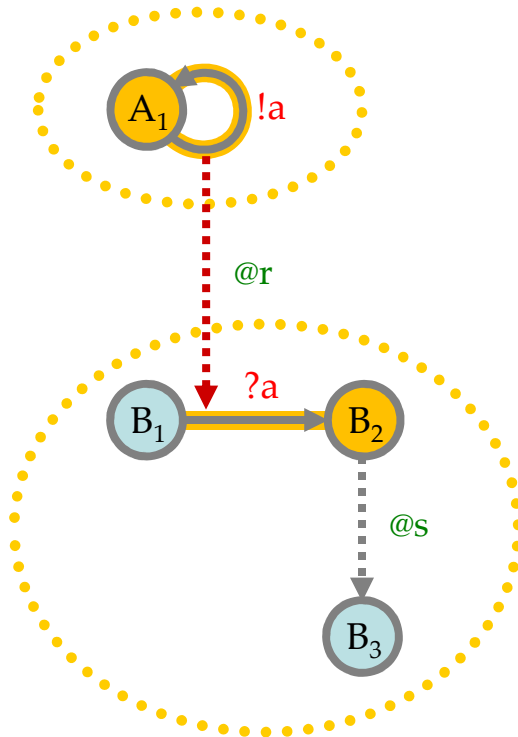


# Interacting Automata

- Current State
- ⋯→ Decay
- Transition
- ⋯→ Interaction

*Kinetic laws:*

*Two complementary actions may result in an interaction.*



- $A_1$  is a *state*
- $a$  is a *channel* i.e. a named *interaction interface* (e.g. a surface patch)
- $?,!$  indicate any *complementarity* of interaction (e.g. charge)
- $?a, !a$  indicate *complementary actions*, joined by an interaction arrow  $\dashrightarrow$
- $@r, @s$  are rates

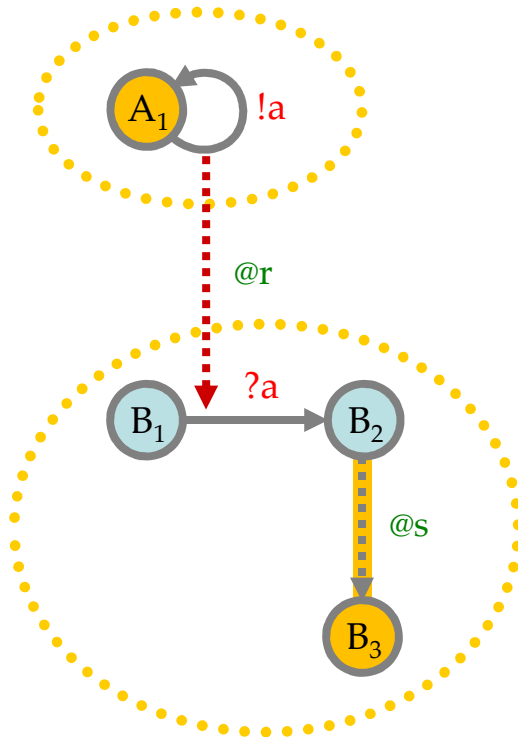
# Interacting Automata

- Current State
- ⋯→ Decay
- Transition
- ⋯→ Interaction

*Kinetic laws:*

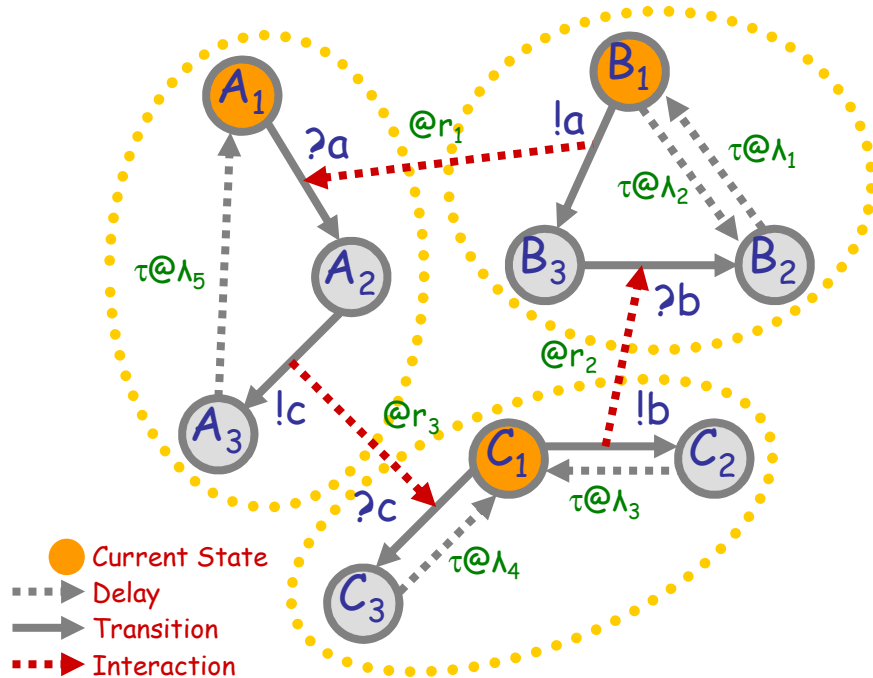
*Two complementary actions may result in an interaction.*

*A decay may happen spontaneously.*



- $A_1$  is a *state*
- $a$  is a *channel* i.e. a named *interaction interface* (e.g. a surface patch)
- $?,!$  indicate any *complementarity* of interaction (e.g. charge)
- $?a, !a$  indicate *complementary actions*, joined by an interaction arrow ⋯→
- $@r, @s$  are *rates*

# Interacting Automata



Interactions have rates. Actions DO NOT have rates.

*The equivalent process algebra model*

```

new a@r1
new b@r2
new c@r3
} Communication channels

A1 = ?a; A2
A2 = !c; A3
A3 = τ@λ5; A1
} Automata

B1 = τ@λ2; B2 + !a; B3
B2 = τ@λ1; B1
B3 = ?b; B2
}

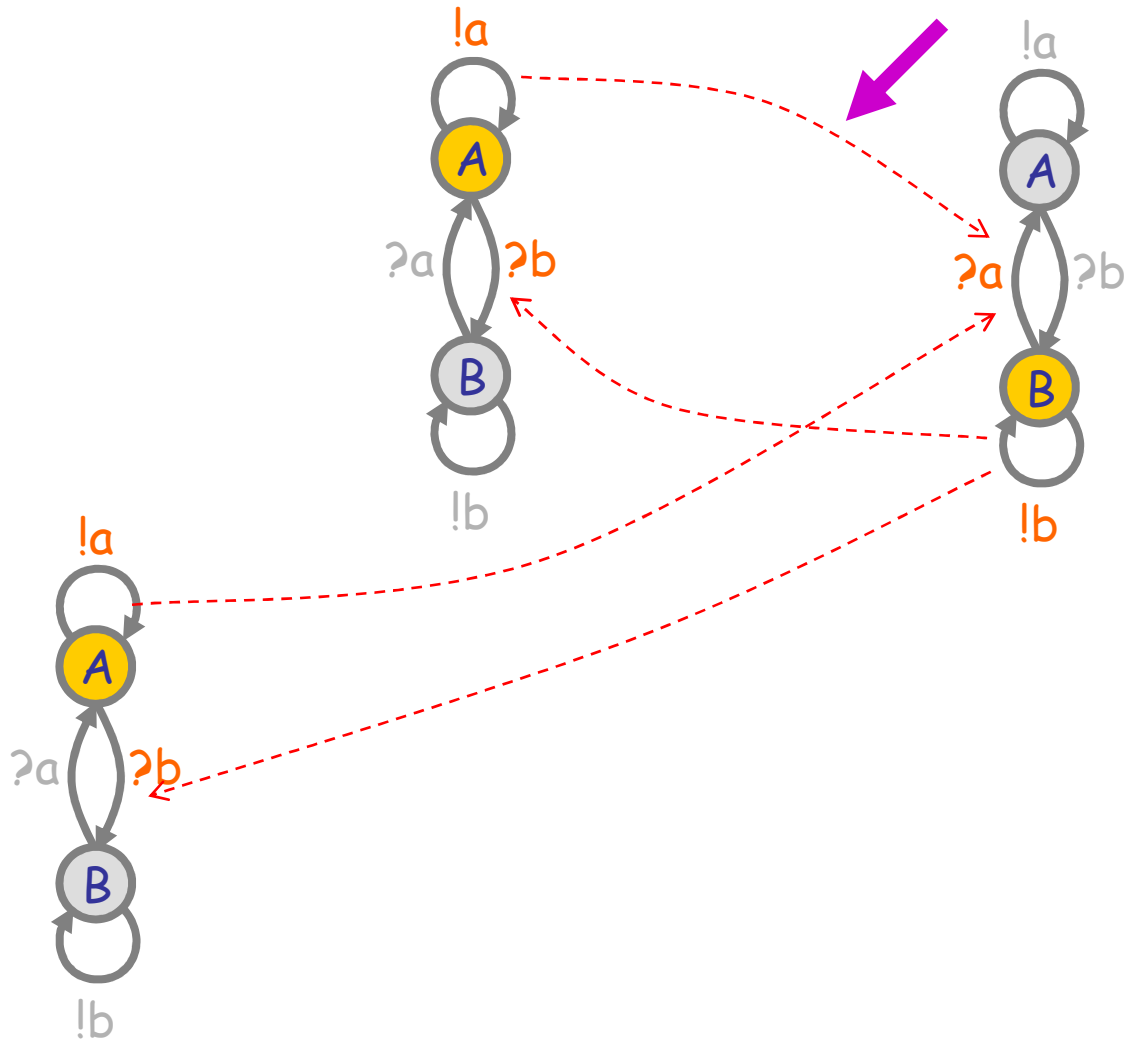
C1 = !b; C2 + ?c; C3
C2 = τ@λ3; C1
C3 = τ@λ4; C2
}

A1 | B1 | C1 } The system and initial state
    
```

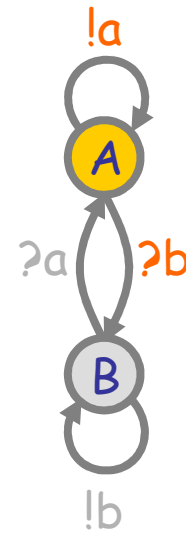
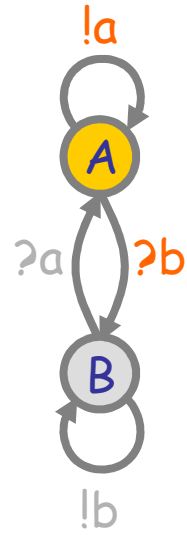
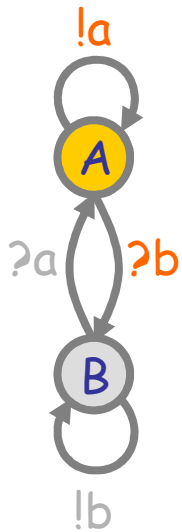




# Interactions in a Population

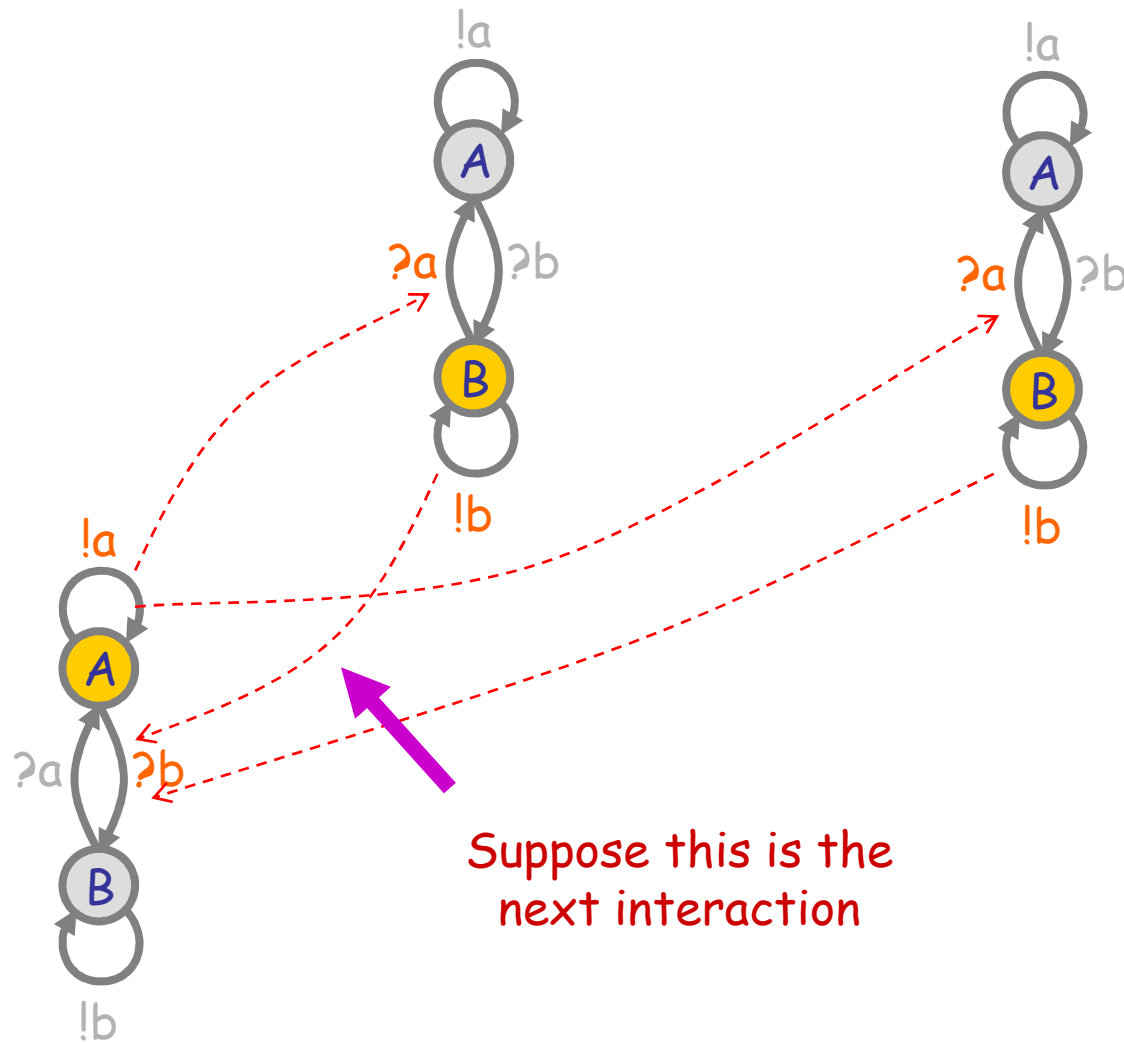


# Interactions in a Population

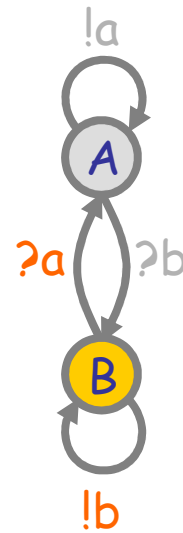
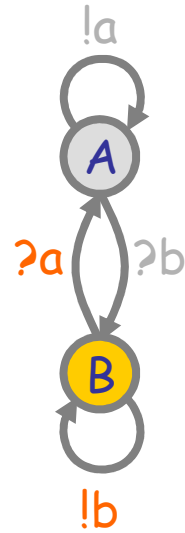
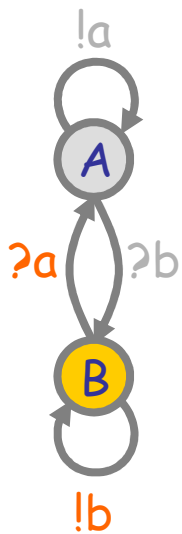


All-A stable population

# Interactions in a Population (2)



# Interactions in a Population (2)

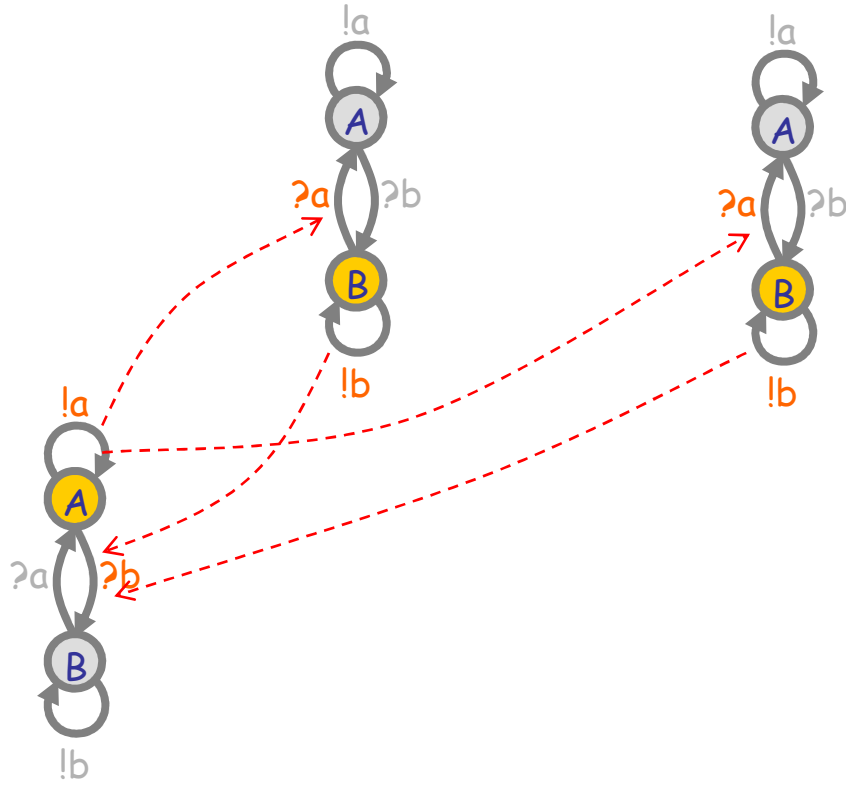


All-B stable population

Nondeterministic population behavior ("multistability")



# CTMC Semantics



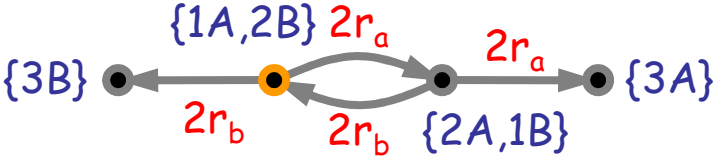
CTMC  
(homogeneous) Continuous Time Markov Chain

- directed graph with no self loops
- nodes are system states
- arcs have transition rates

Probability of holding in state A:

$$\Pr(H_A > t) = e^{-rt}$$

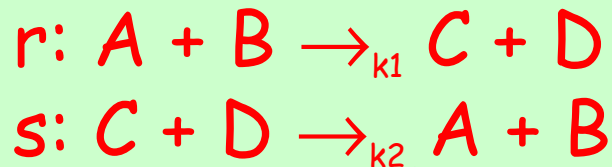
in general,  $\Pr(H_A > t) = e^{-Rt}$  where R is the sum of all the exit rates from A



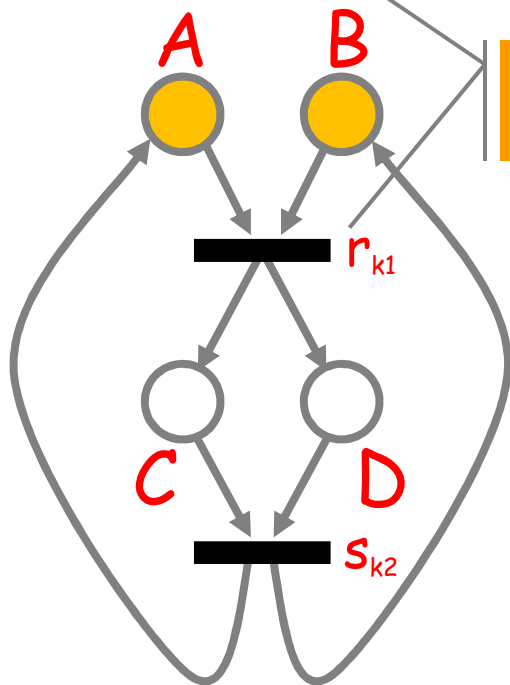
CTMC

# Chemistry vs. Automata

A process algebra (chemistry)



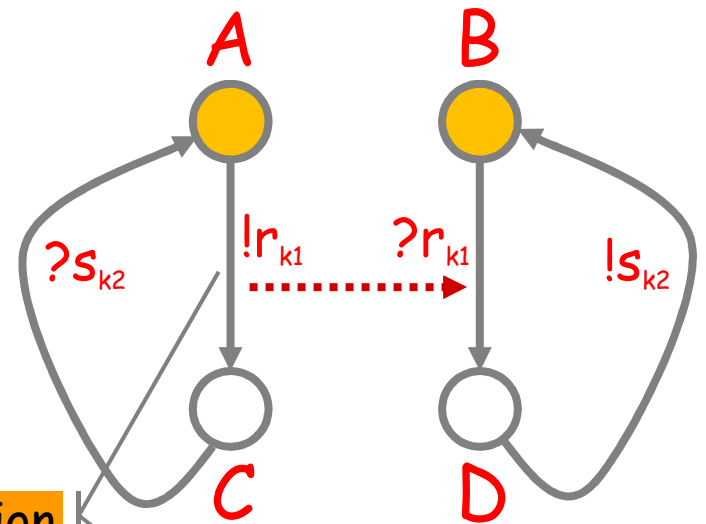
Does A become C or D?



Reaction oriented

1 line per reaction

A different process algebra (automata)



Interaction oriented

1 line per component

$$A = !r_{k_1}; C$$

$$C = ?s_{k_2}; A$$

$$B = ?r_{k_1}; D$$

$$D = !s_{k_2}; B$$

A becomes C not D!

The same "model"

Maps to a CTMC

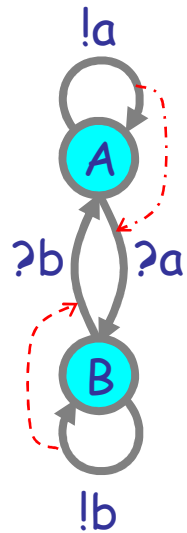
Maps to a CTMC

A Petri-Net-like representation. Precise and dynamic, but not modular, scalable, or maintainable.

A compositional graphical representation (precise, dynamic *and* modular) and the corresponding calculus.

# Groupies and Celebrities

# Groupies and Celebrities



## Celebrity

(does not want to be like somebody else)

```
directive sample 1.0 1000
directive plot A(); B()

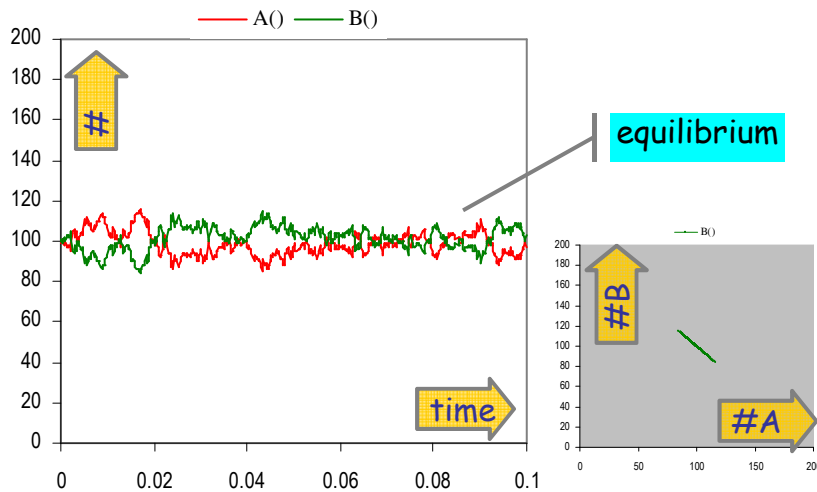
new a@1.0:chan()
new b@1.0:chan()

let A() = do !a; A() or ?a; B()
and B() = do !b; B() or ?b; A()

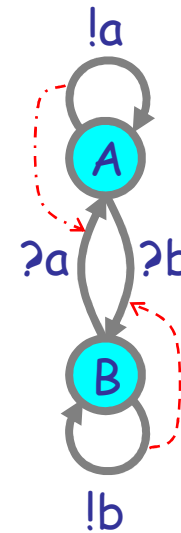
run 100 of (A() | B())
```

a@1.0  
b@1.0

A stochastic collective of celebrities:



Stable because as soon as a A finds itself in the majority, it is more likely to find somebody in the same state, and hence change, so the majority is weakened.



## Groupie

(wants to be like somebody different)

```
directive sample 1.0 1000
directive plot A(); B()

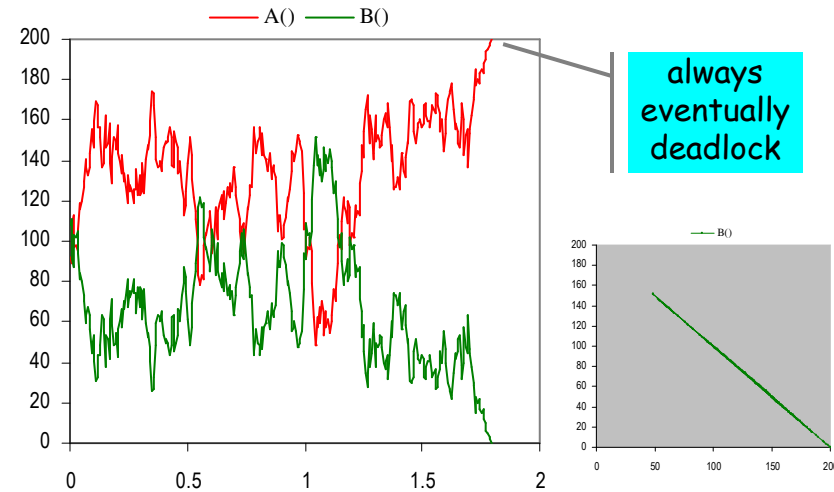
new a@1.0:chan()
new b@1.0:chan()

let A() = do !a; A() or ?b; B()
and B() = do !b; B() or ?a; A()

run 100 of (A() | B())
```

a@1.0  
b@1.0

A stochastic collective of groupies:

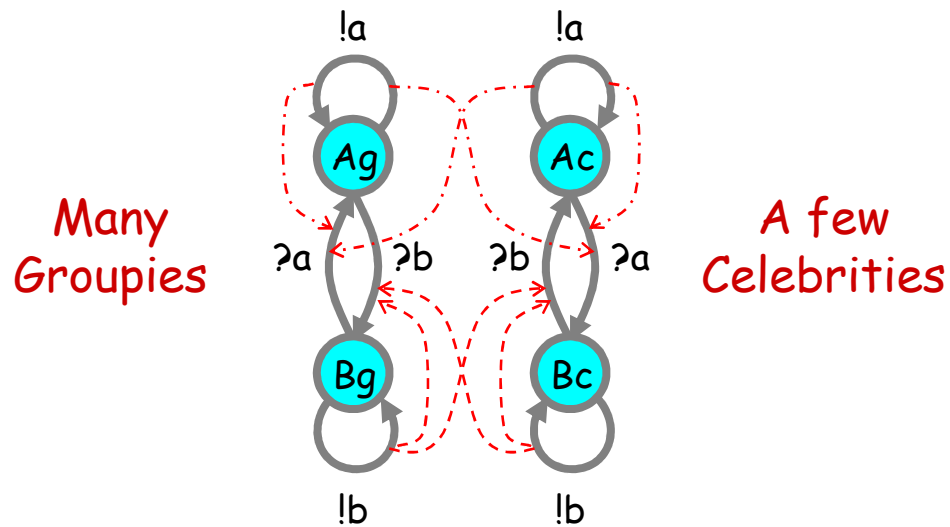


Unstable because within an A majority, an A has difficulty finding a B to emulate, but the few B's have plenty of A's to emulate, so the majority may switch to B. Leads to deadlock when everybody is in the same state and there is nobody different to emulate.



# Both Together

A way to break the deadlocks: Groupies with just a few Celebrities



```
directive sample 10.0
directive plot Ag(); Bg(); Ac(); Bc()

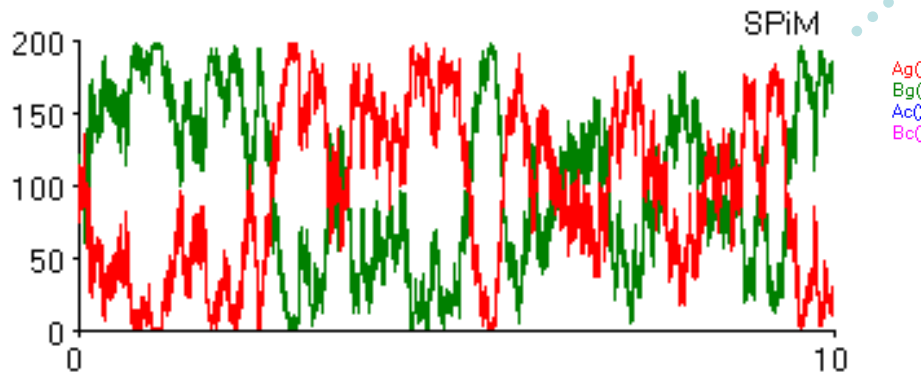
new a@1.0:chan()
new b@1.0:chan()

let Ac() = do !a; Ac() or ?a; Bc()
and Bc() = do !b; Bc() or ?b; Ac()

let Ag() = do !a; Ag() or ?b; Bg()
and Bg() = do !b; Bg() or ?a; Ag()

run 1 of Ac()
run 100 of (Ag() | Bg())
```

never  
deadlock

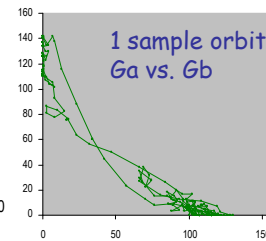
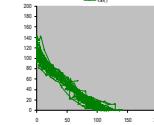
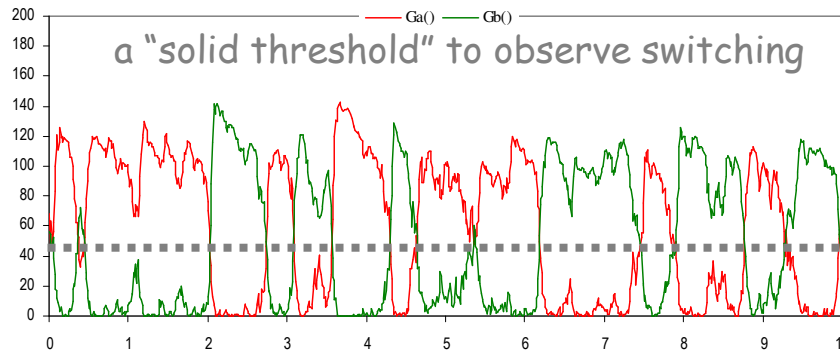
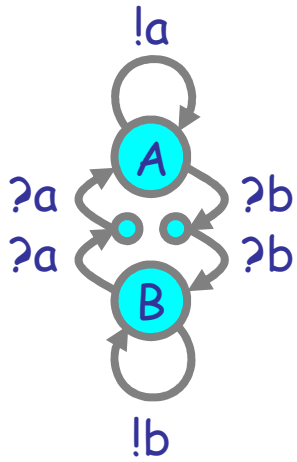


A tiny bit of  
"noise" can make a  
huge difference

Regularity can arise not far from chaos

# Hysteric Groupies

We can get more regular behavior from groupies if they "need more convincing", or "hysteresis" (history-dependence), to switch states.



```
directive sample 10.0 1000
directive plot Ga(); Gb()

new a@1.0:chan()
new b@1.0:chan()

let Ga() = do !a; Ga() or ?b; ?b; Gb()
and Gb() = do !b; Gb() or ?a; ?a; Ga()

let Da() = !a; Da()
and Db() = !b; Db()

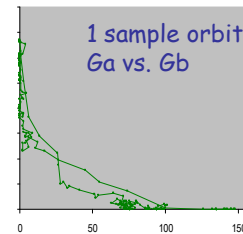
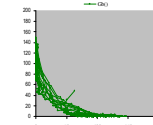
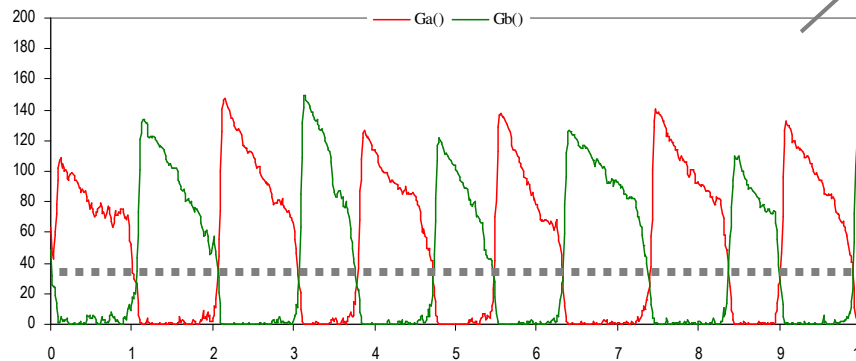
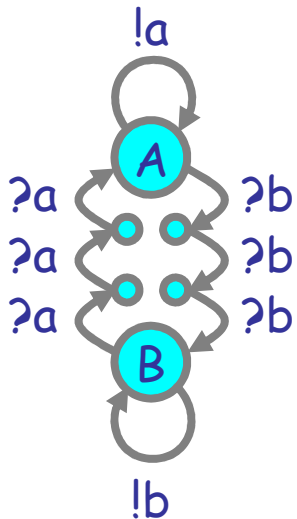
run 100 of (Ga() | Gb())
run 1 of (Da() | Db())
```



(With doping to break deadlocks)

N.B.: It will not oscillate without doping (noise)

"regular" oscillation



```
directive sample 10.0 1000
directive plot Ga(); Gb()

new a@1.0:chan()
new b@1.0:chan()

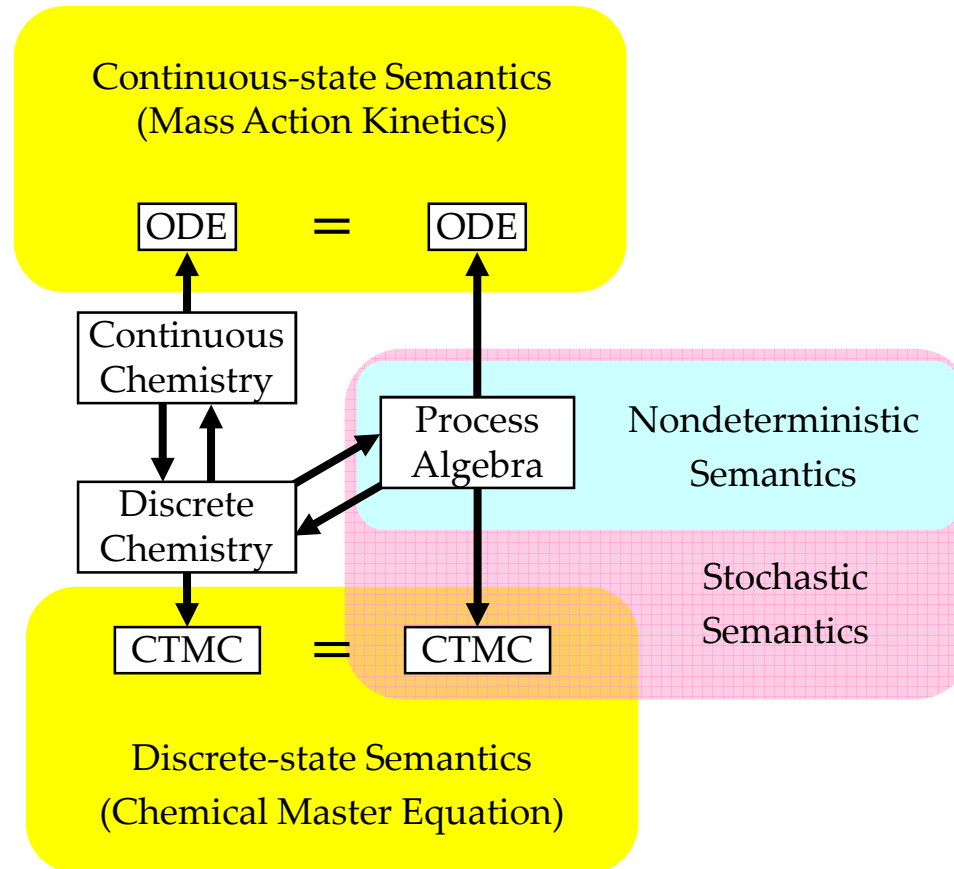
let Ga() = do !a; Ga() or ?b; ?b; ?b; Gb()
and Gb() = do !b; Gb() or ?a; ?a; ?a; Ga()

let Da() = !a; Da()
and Db() = !b; Db()

run 100 of (Ga() | Gb())
run 1 of (Da() | Db())
```

# Semantics of Collective Behavior

# The Two Semantic Sides of Chemistry

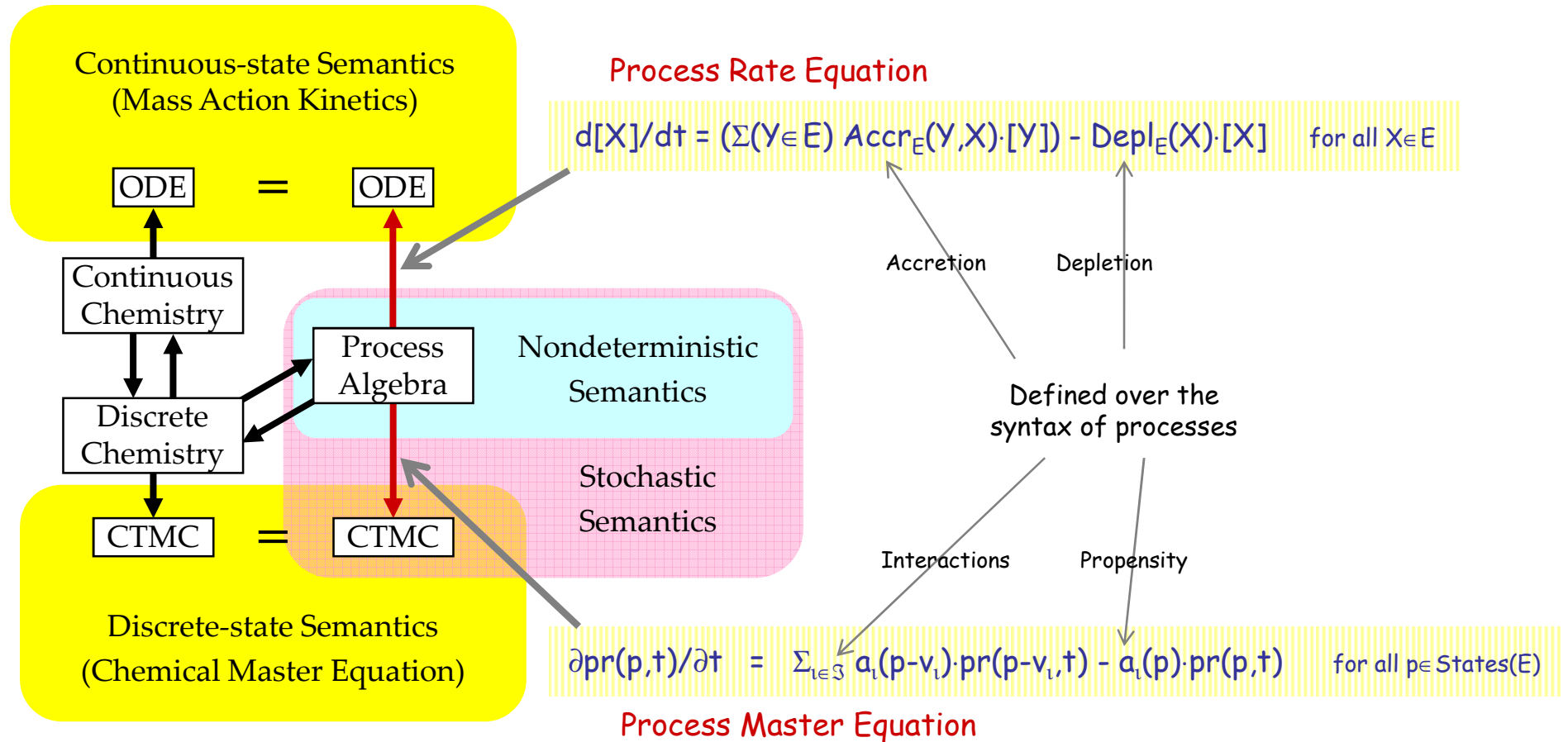


These diagrams commute via appropriate maps.

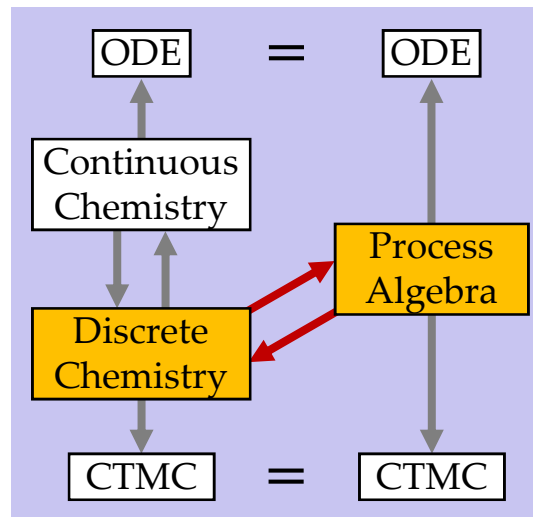
L. Cardelli: "On Process Rate Semantics" (TCS)

L. Cardelli: "A Process Algebra Master Equation" (QEST'07)

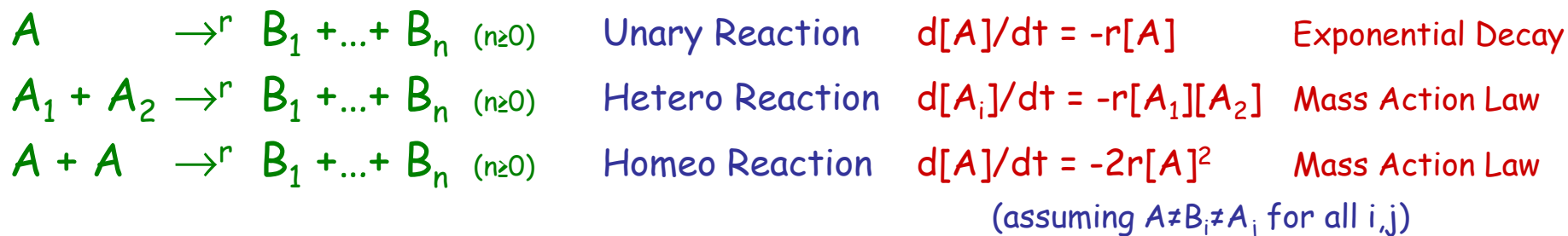
# Quantitative Process Semantics



# Stochastic Processes & Discrete Chemistry



# Chemical Reactions



No other reactions!

JOURNAL OF CHEMICAL PHYSICS

VOLUME 113, NUMBER 1

## The chemical Langevin equation

Daniel T. Gillespie<sup>a)</sup>  
 Research Department, Code 4T4100D, Naval Air Warfare Center, China Lake, California 93555

Genuinely *trimolecular* reactions do not physically occur in dilute fluids with any appreciable frequency. *Apparently* trimolecular reactions in a fluid are usually the combined result of two bimolecular reactions and one monomolecular reaction, and involve an additional short-lived species.

## Chapter IV: Chemical Kinetics

[David A. Reckhow, CEE 572 Course]

... reactions may be either elementary or non-elementary. Elementary reactions are those reactions that occur exactly as they are written, without any intermediate steps. These reactions **almost always involve just one or two reactants**. ... Non-elementary reactions involve a series of two or more elementary reactions. Many complex environmental reactions are non-elementary. In general, **reactions with an overall reaction order greater than two, or reactions with some non-integer reaction order are non-elementary**.

## THE COLLISION THEORY OF REACTION RATES

[www.chemguide.co.uk](http://www.chemguide.co.uk)

The chances of all this happening if your reaction needed a collision involving more than 2 particles are remote. All three (or more) particles would have to arrive at exactly the same point in space at the same time, with everything lined up exactly right, and having enough energy to react. That's not likely to happen very often!

Trimolecular reactions:



the measured "r" is an (imperfect) aggregate of e.g.:



Enzymatic reactions:



the "r" is given by Michaelis-Menten (approximated steady-state) laws:



Reactions have rates. Molecules do not have rates.

# Chemical Ground Form (CGF)

$E ::= 0 : X=M, E$

Reagents

$M ::= 0 : \pi; P \oplus M$

Molecules

$P ::= 0 : X | P$

Solutions

$\pi ::= \tau_{(r)} : ?a_{(r)} : !a_{(r)}$

Actions (delay, input, output)

$CGF ::= E, P$

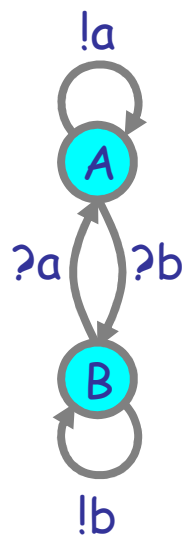
Reagents plus Initial Conditions

A stochastic subset of CCS  
(no values, no restriction)

Interacting Automata  
+ dynamic forking

(To translate chemistry to processes we need a bit more than interacting automata: we may have "+" on the right of  $\rightarrow$ , that is we may need "|" after  $\pi$ .)

$\oplus$  is stochastic choice (vs. + for chemical reactions)  
0 is the null solution ( $P|0 = 0|P = P$ )  
and null molecule ( $M \oplus 0 = 0 \oplus M = M$ )  
Each  $X$  in  $E$  is a distinct *species*  
Each name  $a$  is assigned a fixed rate  $r: a_{(r)}$



Ex: Interacting Automata

(= finite-control CGFs: they use "|" only in initial conditions):

$A = !a; A \oplus ?b; B$

Automaton in state A

$B = !b; B \oplus ?a; A$


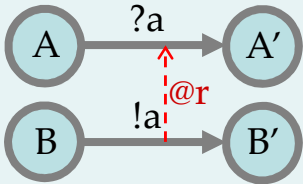
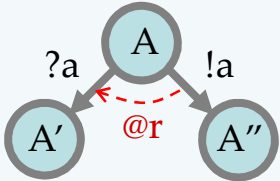
Automaton in state B

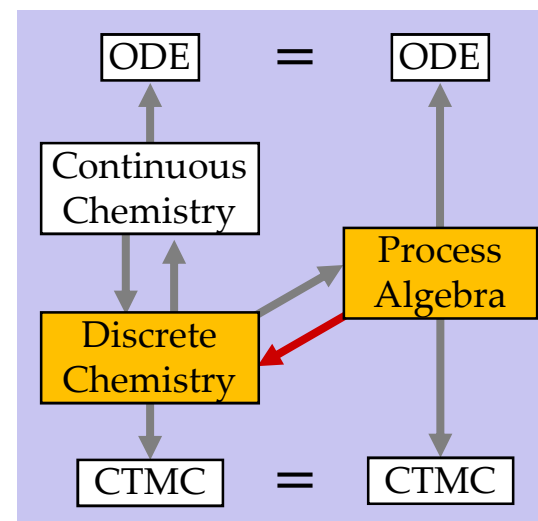
$A|A|B|B$

Initial conditions:  
2A and 2B

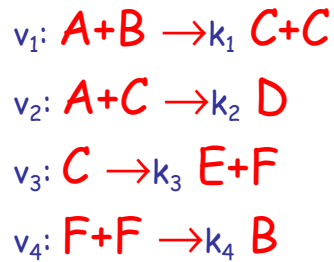


# From Reagents to Reactions (by example)

Interacting Automata	Discrete Chemistry
initial states $A \mid A \mid \dots \mid A$	initial quantities $\#A_0$
	$A \xrightarrow{r} A'$
	$A+B \xrightarrow{r} A'+B'$
	$A+A \xrightarrow{2r} A'+A''$



# From Reactions to Reagents (by example)

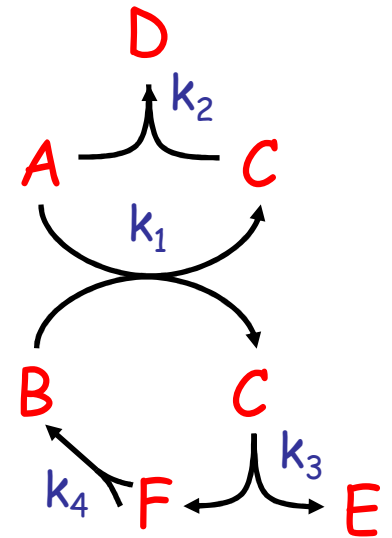


Interaction Matrix

channels and rates  
(1 per reaction)

Half-rate for homeo reactions

	$v_1(k_1)$	$v_2(k_2)$	$v_3(k_3)$	$v_4(k_4/2)$
A	?:(C C)	?:D		
B	!:0			
C		!:0	$\tau:(E F)$	
D				
E				
F				?:B !:0



1: Fill the matrix by columns:

Degradation reaction  $v_i: X \xrightarrow{k_i} P_i$   
add  $\tau:P_i$  to  $\langle X, v_i \rangle$ .

Hetero reaction  $v_i: X+Y \xrightarrow{k_i} P_i$   
add  $?:P_i$  to  $\langle X, v_i \rangle$  and  $!:0$  to  $\langle Y, v_i \rangle$

Homeo reaction  $v_i: X+X \xrightarrow{k_i} P_i$   
add  $?:P_i$  and  $!:0$  to  $\langle X, v_i \rangle$

definitions  
(1 per species)

2: Read the result by rows:

$$A = ?v_{1(k_1)}:(C|C) \oplus ?v_{2(k_2)}:D$$

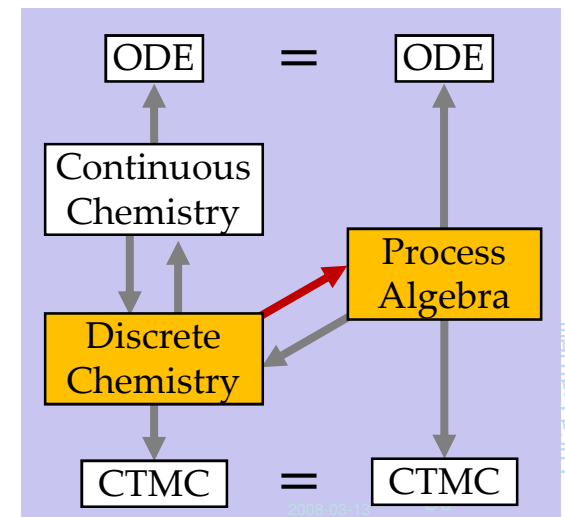
$$B = !v_{1(k_1)}:0$$

$$C = !v_{2(k_2)}:0 \oplus \tau_{k_3}:(E|F)$$

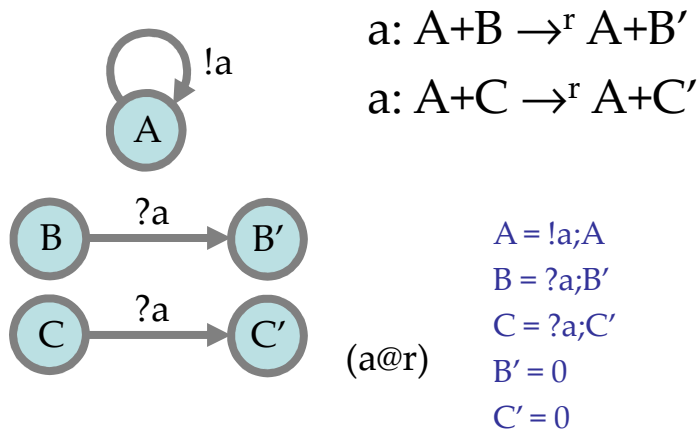
$$D = 0$$

$$E = 0$$

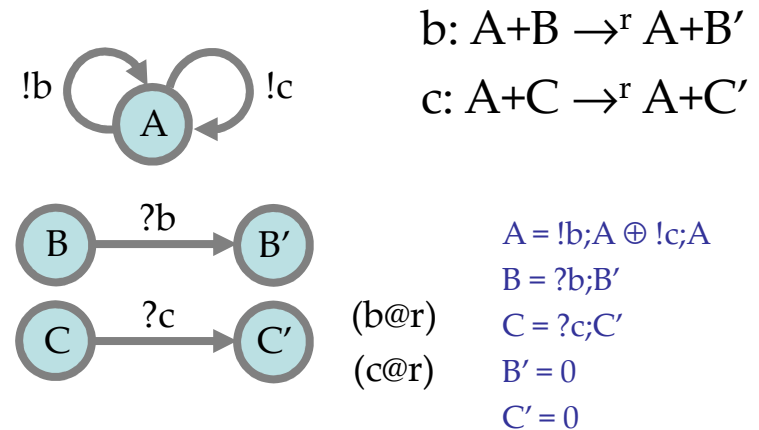
$$F = ?v_{4(k_4/2)}:B \oplus !v_{4(k_4/2)}:0$$



# Entangled vs Detangled



Entangled: Two reactions on one channel



Detangled: Two reactions on two separate channels

We need a semantics of automata that identifies automata that have the "same chemistry".

No process algebra equivalence is like this!

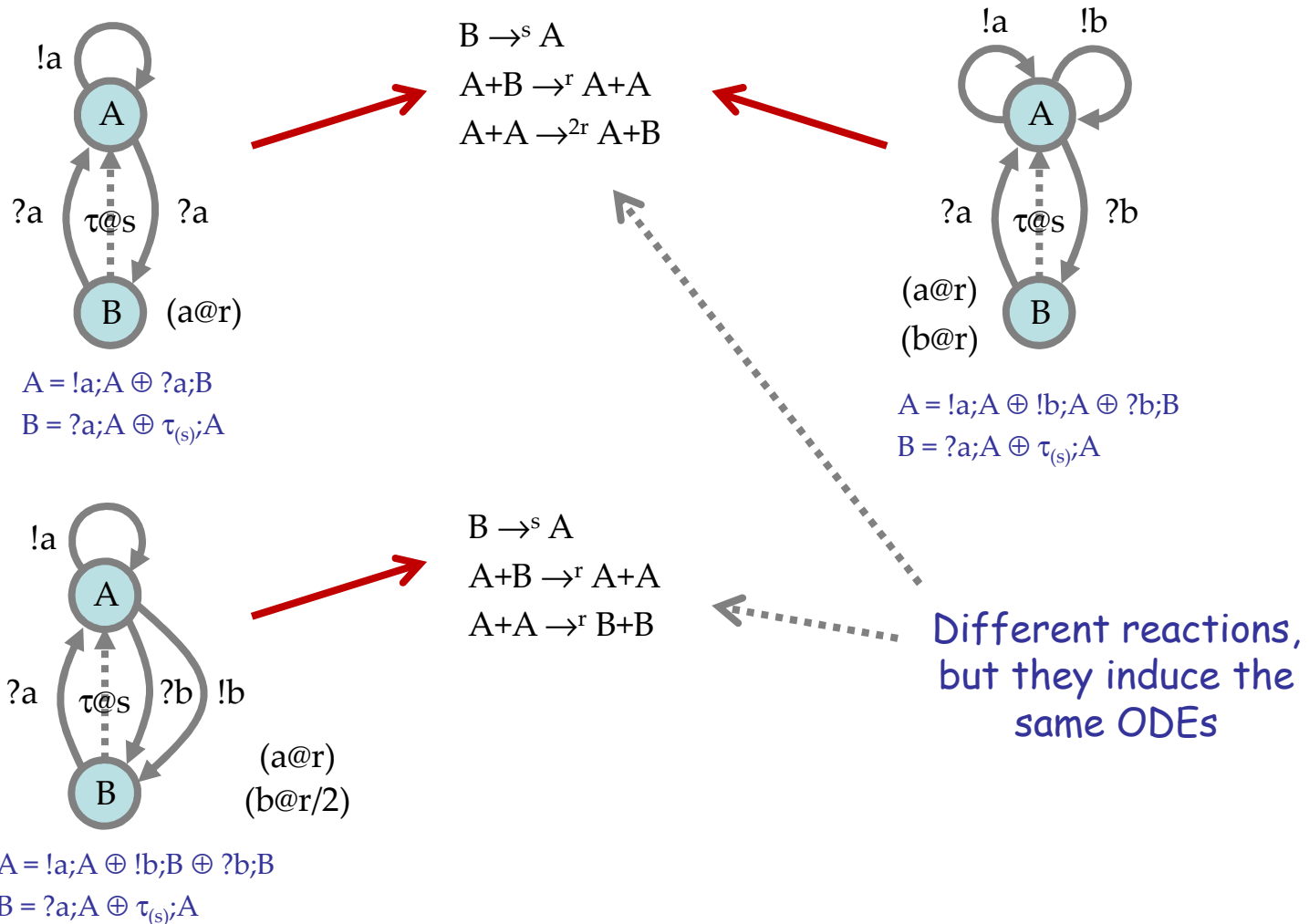
Entangled automata lead to more compact models than in chemistry.

Detangled automata are in simple correspondence with chemistry.

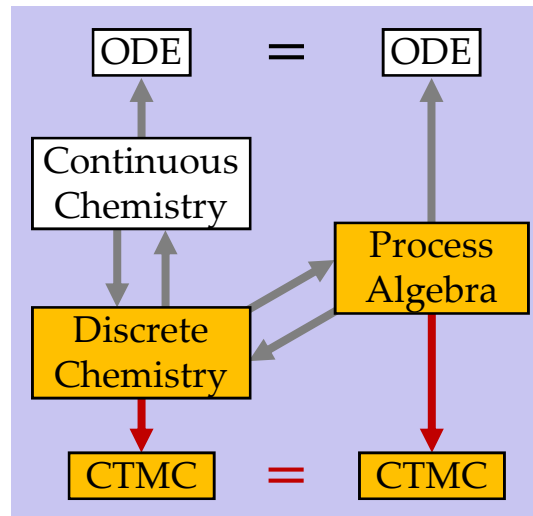
# Same Semantics

Could chemistry itself be that semantics?

No: different sets of reactions can have the same behavior!

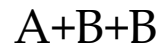
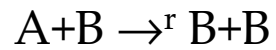
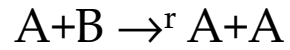


# Discrete-State Semantics

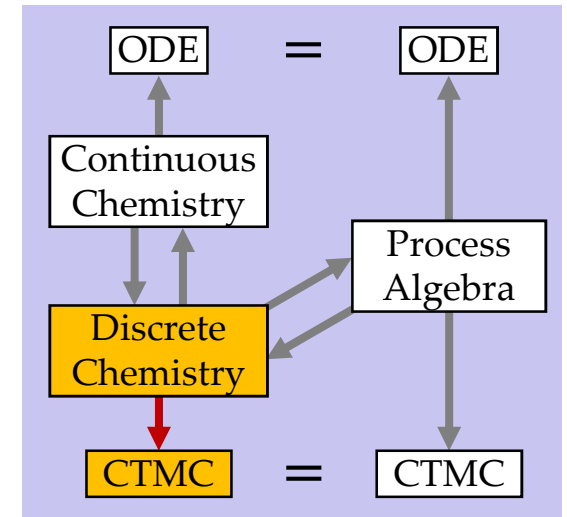
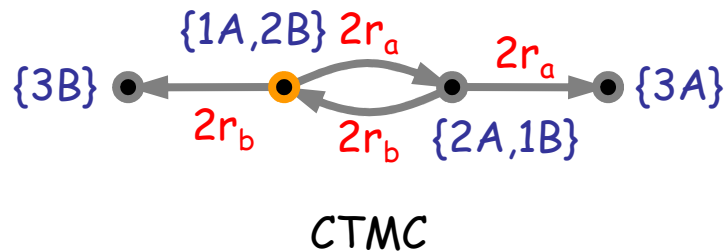


# Discrete Semantics of Reactions

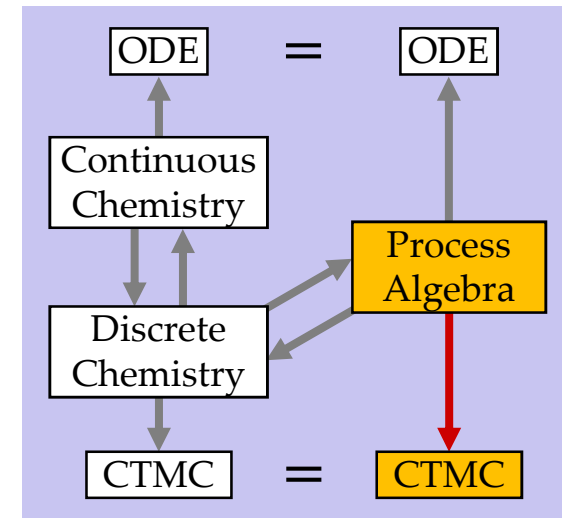
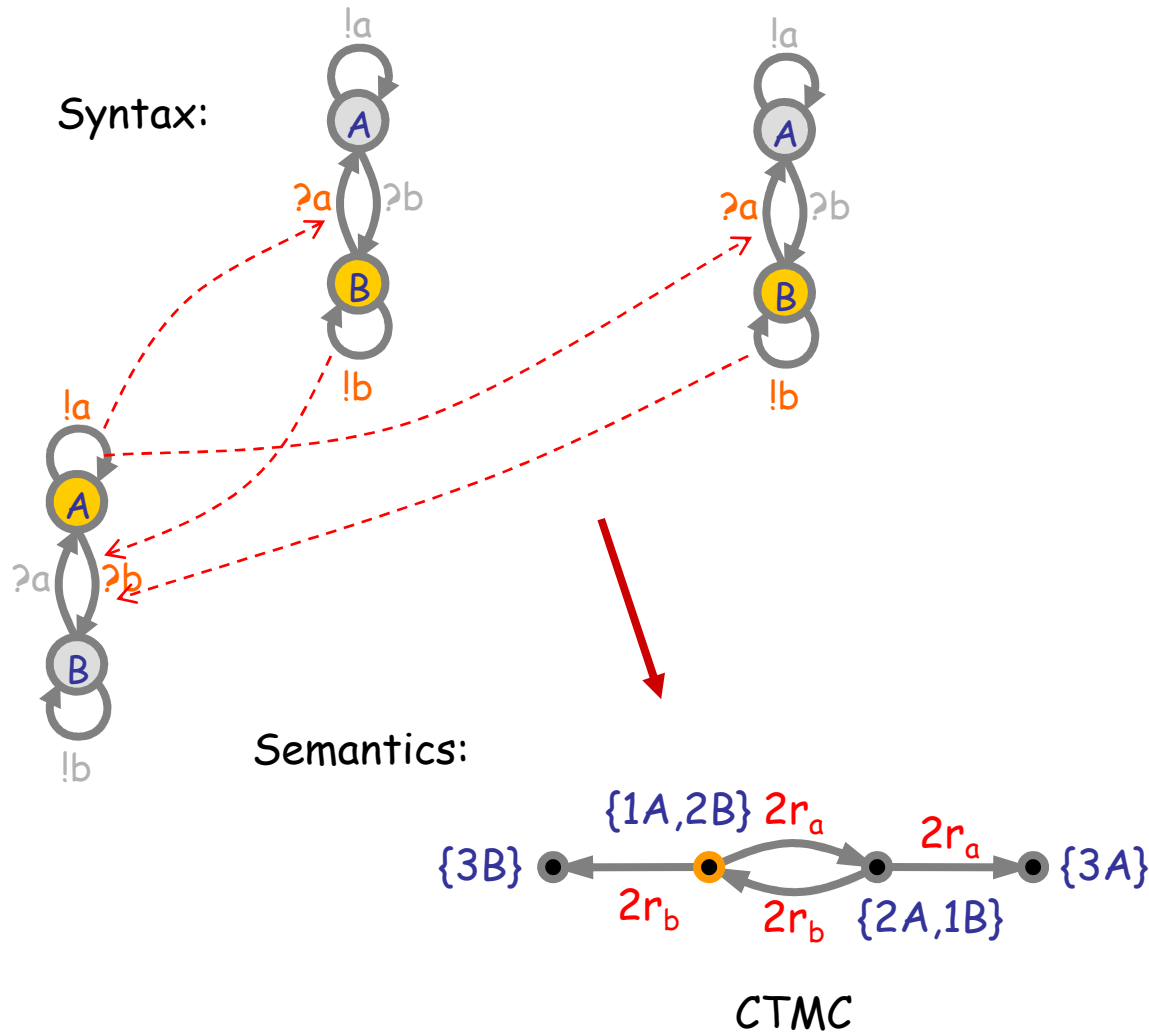
Syntax:



Semantics:



# Discrete Semantics of Reagents

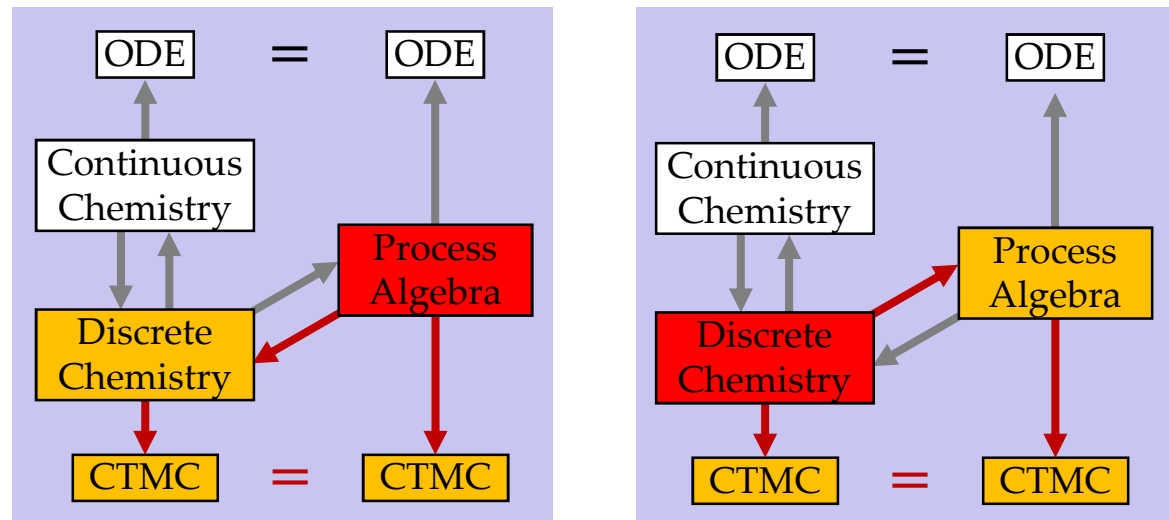


# Discrete State Equivalence

- Def:  $\approx$  is equivalent CTMC's (isomorphic graphs with same rates).

- Thm:  $E \approx \text{Ch}(E)$

- Thm:  $C \approx \text{Pi}(C)$



- For each  $E$  there is an  $E' \approx E$  that is detangled ( $E' = \text{Pi}(\text{Ch}(E))$ )

- For each  $E$  in automata form there is an  $E' \approx E$  that is detangled and in automata form ( $E' = \text{Detangle}(E)$ ).

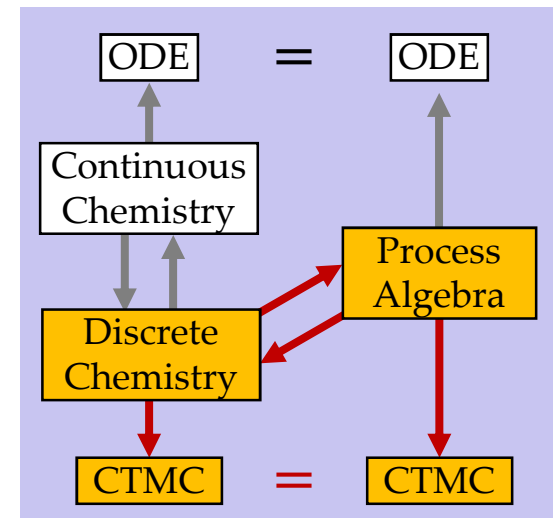


# Process Algebra = Discrete Chemistry

This is enough to establish that the process algebra is really faithful to the chemistry.

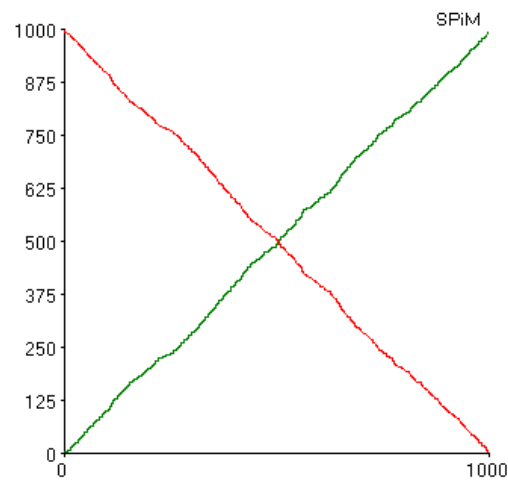
But CTMC are not the “ultimate semantics” because there are still questions of when two different CTMCs are actually equivalent (e.g. “lumping”).

The “ultimate semantics” of chemistry is the *Chemical Master Equation* (derivable from the Chapman-Kolmogorov equation of the CTMC).

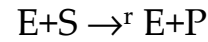
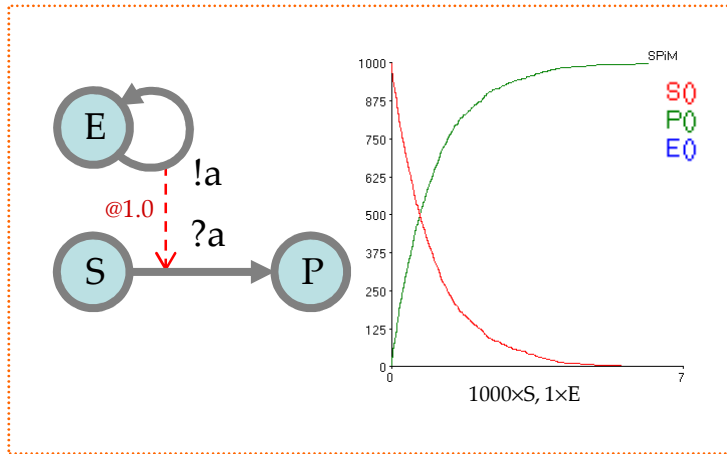


# Exercise: Making Lines

Or: build me a population like this:



# Second-order and Zero-order Regime



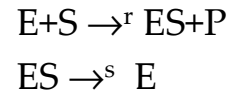
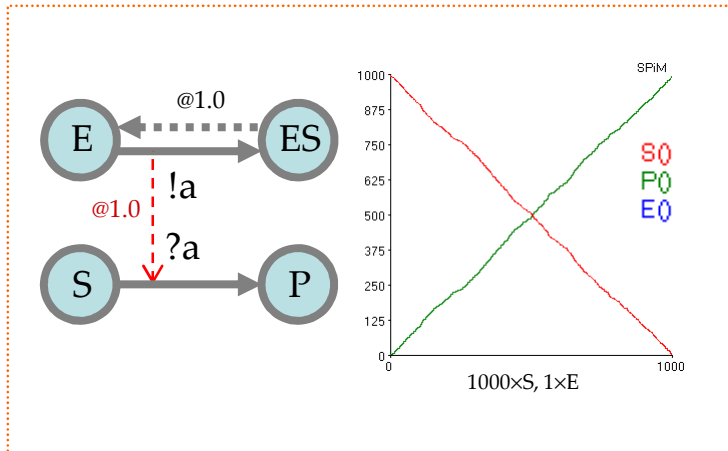
```
directive sample 1000.0
directive plot S(); P(); E()
```

```
new a@1.0:chan()
```

```
let E() = !a; E()
and S() = ?a; P()
and P() = ()
```

```
run (1 of E() | 1000 of S())
```

Second-Order Regime  
 $[S]^* = -r[E][S]$



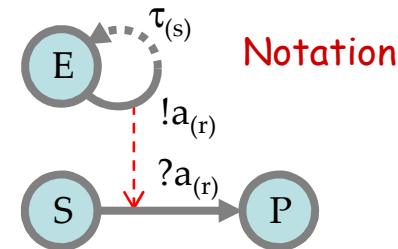
```
directive sample 1000.0
directive plot S(); P(); E()
```

```
new a@1.0:chan()
```

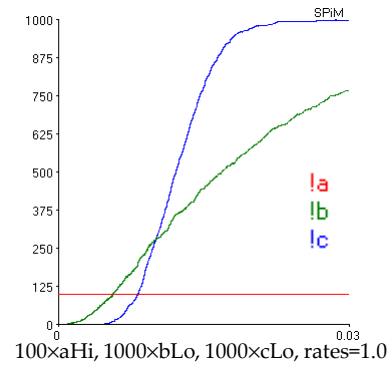
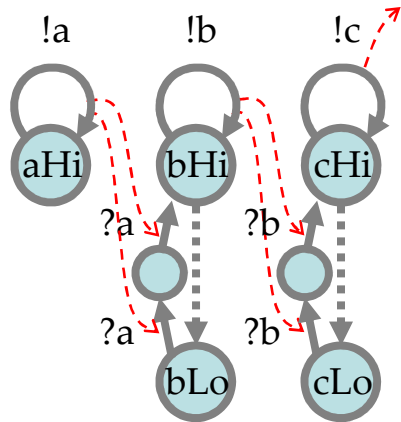
```
let E() = !a; delay@1.0; E()
and S() = ?a; P()
and P() = ()
```

```
run (1 of E() | 1000 of S())
```

Zero-Order Regime  
 $[S]^* \cong -1$  (by assuming  $[ES]^* = 0$ )



# Cascades



Second-Order Regime cascade:  
a signal amplifier (MAPK)  
 $a_{Hi} > 0 \Rightarrow c_{Hi} = \max$

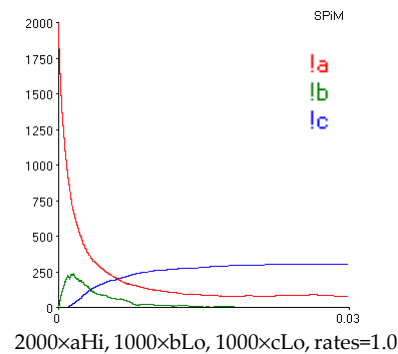
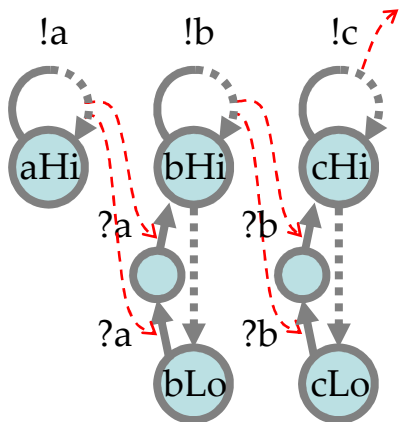
```
directive sample 0.03
directive plot !a: !b: !c

new a@1.0:chan new b@1.0:chan new c@1.0:chan

let Amp_hi(a:chan, b:chan) =
do !b: delay@1.0: Amp_hi(a,b) or delay@1.0: Amp_lo(a,b)
and Amp_lo(a:chan, b:chan) =
?a: ?a: Amp_hi(a,b)

run 1000 of (Amp_lo(a,b) | Amp_lo(b,c))

let A() = !a: A()
run 100 of A()
```



Zero-Order Regime cascade:  
a signal divider!  
 $a_{Hi} = \max \Rightarrow c_{Hi} = 1/3 \max$

```
directive sample 0.03
directive plot !a: !b: !c

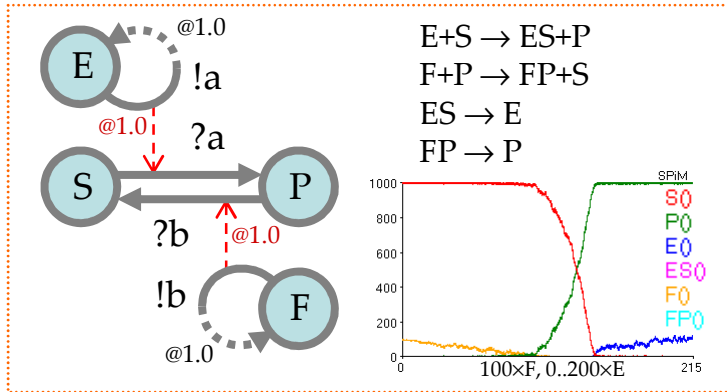
new a@1.0:chan new b@1.0:chan new c@1.0:chan

let Amp_hi(a:chan, b:chan) =
do !b: delay@1.0: Amp_hi(a,b) or delay@1.0: Amp_lo(a,b)
and Amp_lo(a:chan, b:chan) =
?a: ?a: Amp_hi(a,b)

run 1000 of (Amp_lo(a,b) | Amp_lo(b,c))

let A() = !a: delay@1.0: A()
run 2000 of A()
```

# Ultrasensitivity



```

directive sample 215.0
directive plot S(): P(): E(): ES(): F(): FP()

new a@1.0:chan() new b@1.0:chan()

let S() = ?a: P()
and P() = ?b: S()

let E() = !a: delay@1.0: E()
and F() = !b: delay@1.0: F()

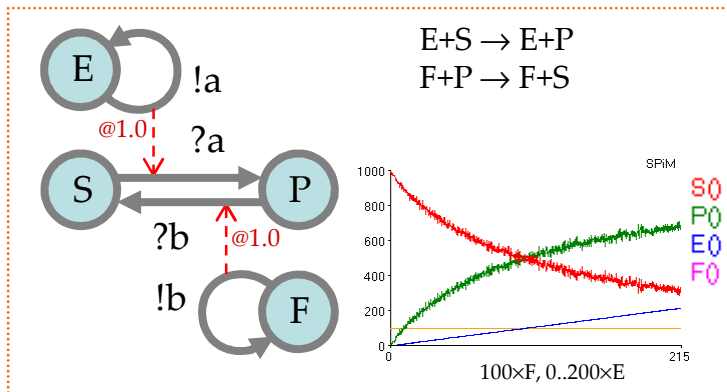
run 1000 of S()

let clock(t:float, tick:chan) = (* sends a tick every t time *)
(val ti = 1/100.0 val d = 1.0/ti (* by 100-step erlang timers *))
let step(n:int) = if n<=0 then !tick: clock(t,tick) else delay@d: step(n-1)
run step(100))

let Sig(p:proc(), tick:chan) = (p() | ?tick: Sig(p,tick))
let raising(p:proc(), t:float) =
(new tick:chan run (clock(t,tick) | Sig(p,tick)))

run 100 of F()
run raising(E,1.0)
    
```

Zero-Order Regime  
A small E-F imbalance causes a much larger S-P switch.



```

directive sample 215.0 1000
directive plot S(): P(): E(): F()

new a@1.0:chan() new b@1.0:chan()

let S() = ?a: P()
and P() = ?b: S()

let E() = !a: E()
and F() = !b: F()

run 1000 of S()

let clock(t:float, tick:chan) = (* sends a tick every t time *)
(val ti = 1/100.0 val d = 1.0/ti (* by 100-step erlang timers *))
let step(n:int) = if n<=0 then !tick: clock(t,tick) else delay@d: step(n-1)
run step(100))

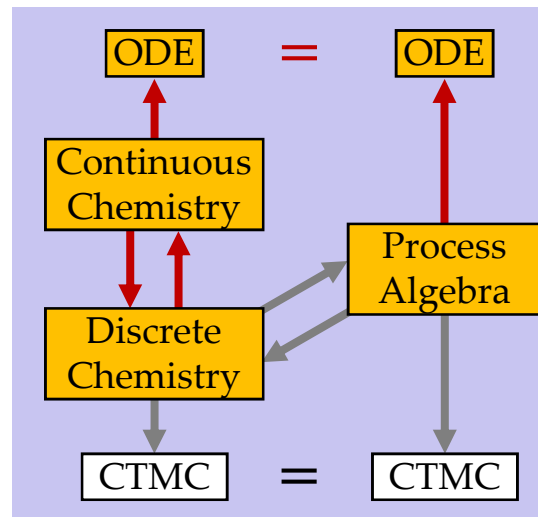
let Sig(p:proc(), tick:chan) = (p() | ?tick: Sig(p,tick))
let raising(p:proc(), t:float) =
(new tick:chan run (clock(t,tick) | Sig(p,tick)))

run 100 of F()
run raising(E,1.0)
    
```

Second-Order Regime

# Continuous-State Semantics

(short version)



# The Gillespie(?) Conversion

Discrete Chemistry	Continuous Chemistry	$\gamma = N_A V$	$:M^{-1}$
initial quantities $\#A_0$	initial concentrations $[A]_0$	with $[A]_0 = \#A_0/\gamma$	
$A \xrightarrow{r} A'$	$A \xrightarrow{k} A'$	with $k = r$	$:s^{-1}$
$A+B \xrightarrow{r} A'+B'$	$A+B \xrightarrow{k} A'+B'$	with $k = r\gamma$	$:M^{-1}s^{-1}$
$A+A \xrightarrow{r} A'+A''$	$A+A \xrightarrow{k} A'+A''$	with $k = r\gamma/2$	$:M^{-1}s^{-1}$

$V$  = interaction volume

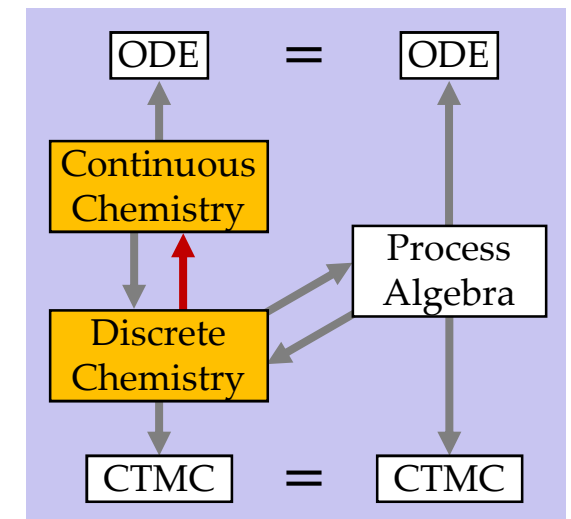
$N_A$  = Avogadro's number

Think  $\gamma = 1$

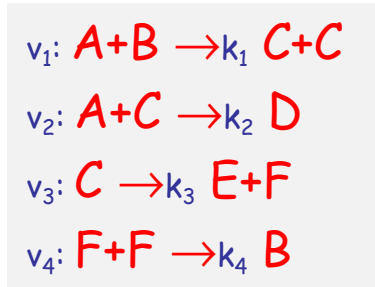
i.e.  $V = 1/N_A$

$M = mol \cdot L^{-1}$

molarity (concentration)



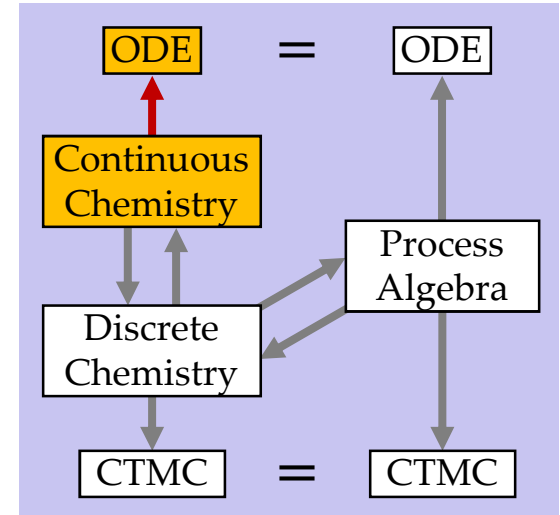
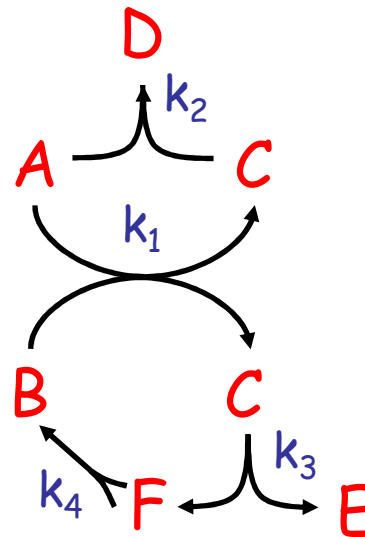
# From Reactions to ODEs



Write the coefficients by columns

Stoichiometric Matrix

	reactions	$v_1$	$v_2$	$v_3$	$v_4$
species	N				
	A	-1	-1		
	B	-1			1
	C	2	-1	-1	
	D		1		
	E			1	
	F			1	-2



Quantity changes

Stoichiometric matrix

Rate laws

$$d[X]/dt = N \cdot I$$

$$\begin{aligned}
 d[A]/dt &= -I_1 - I_2 \\
 d[B]/dt &= -I_1 + I_4 \\
 d[C]/dt &= 2I_1 - I_2 - I_3 \\
 d[D]/dt &= I_2 \\
 d[E]/dt &= I_3 \\
 d[F]/dt &= I_3 - 2I_4
 \end{aligned}$$

Read the concentration changes from the rows

E.g.  $d[A]/dt = -k_1[A][B] - k_2[A][C]$

Set a rate law for each reaction (Degradation/Hetero/Homeo)

	I
$I_1$	$k_1[A][B]$
$I_2$	$k_2[A][C]$
$I_3$	$k_3[C]$
$I_4$	$k_4[F]^2$

**X**: chemical species  
**[-]**: quantity of molecules  
**I**: rate laws  
**k**: kinetic parameters  
**N**: stoichiometric matrix



# Processes Rate Equation

Process Rate Equation for Reagents E in volume  $\gamma$

$$d[X]/dt = (\sum_{Y \in E} \text{Accr}_E(Y, X) \cdot [Y]) - \text{Depl}_E(X) \cdot [X]$$

for all  $X \in E$

"The change in process concentration (!!) for X at time t is:  
 the sum over all possible (kinds of) processes Y of:  
 the concentration at time t of Y  
 times the accretion from Y to X  
 minus the concentration at time t of X  
 times the depletion of X to some other Y"

$\text{Depl}_E(X) =$

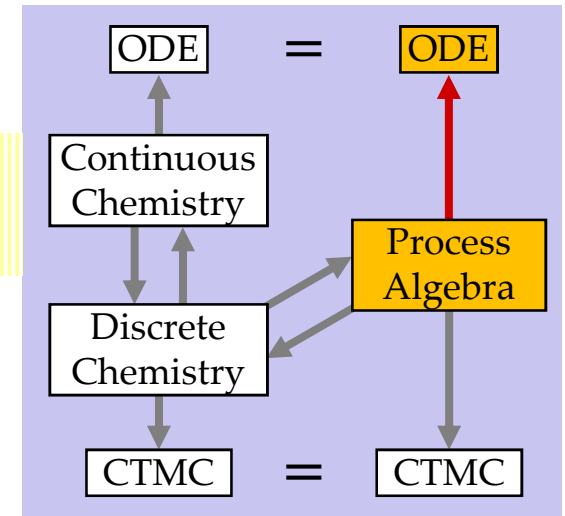
$$\begin{aligned} & \sum_{i: E.X.i=\tau_{(r)};P} r + \\ & \sum_{i: E.X.i=?a_{(r)};P} r\gamma \cdot \text{OutsOn}_E(a) + \\ & \sum_{i: E.X.i=!a_{(r)};P} r\gamma \cdot \text{InsOn}_E(a) \end{aligned}$$

$\text{Accr}_E(Y, X) =$

$$\begin{aligned} & \sum_{i: E.Y.i=\tau_{(r)};P} \#X(P) \cdot r + \\ & \sum_{i: E.Y.i=?a_{(r)};P} \#X(P) \cdot r\gamma \cdot \text{OutsOn}_E(a) + \\ & \sum_{i: E.Y.i=!a_{(r)};P} \#X(P) \cdot r\gamma \cdot \text{InsOn}_E(a) \end{aligned}$$

$\text{InsOn}_E(a) = \sum_{Y \in E} \#\{Y.i \mid E.Y.i=?a_{(r)};P\} \cdot [Y]$

$\text{OutsOn}_E(a) = \sum_{Y \in E} \#\{Y.i \mid E.Y.i=!a_{(r)};P\} \cdot [Y]$



$$X = \tau_{(r)};0 \quad \rightarrow \quad d[X]/dt = -r[X]$$

$$\begin{aligned} X = ?a_{(r)};0 \\ Y = !a_{(r)};0 \end{aligned} \quad \rightarrow \quad \begin{aligned} d[X]/dt &= -r\gamma[X][Y] \\ d[Y]/dt &= -r\gamma[X][Y] \end{aligned}$$

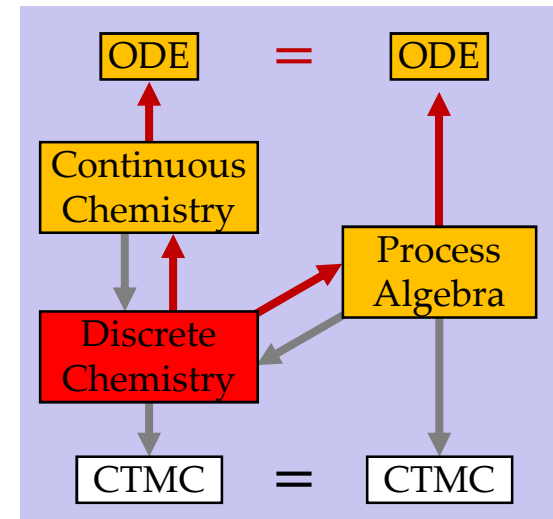
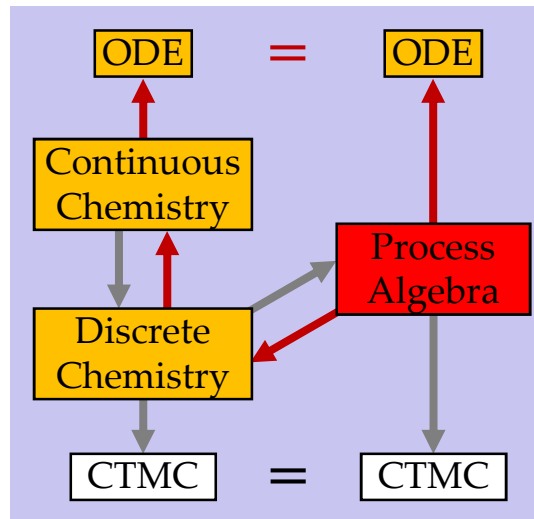
$$\begin{aligned} X = ?a_{(r)};0 \\ \oplus !a_{(r)};0 \end{aligned} \quad \rightarrow \quad d[X]/dt = -2r\gamma[X]^2$$

# Continuous State Equivalence

- Def:  $\approx$  is equivalence of polynomials over the field of reals.

- Thm:  $E \approx \text{Cont}(\text{Ch}(E))$

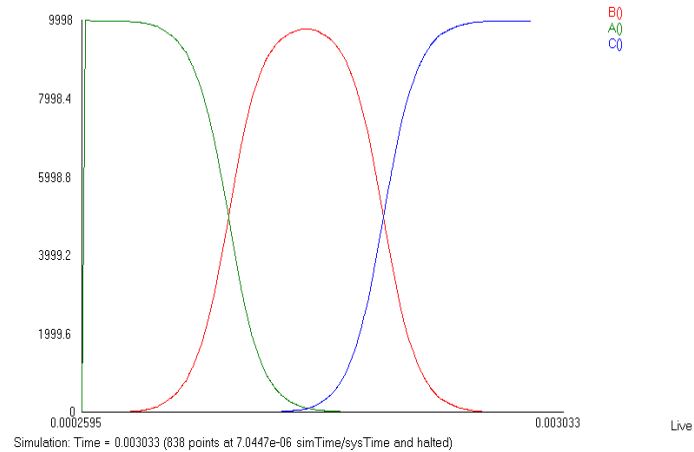
- Thm:  $\text{Cont}(C) \approx \text{Pi}(C)$



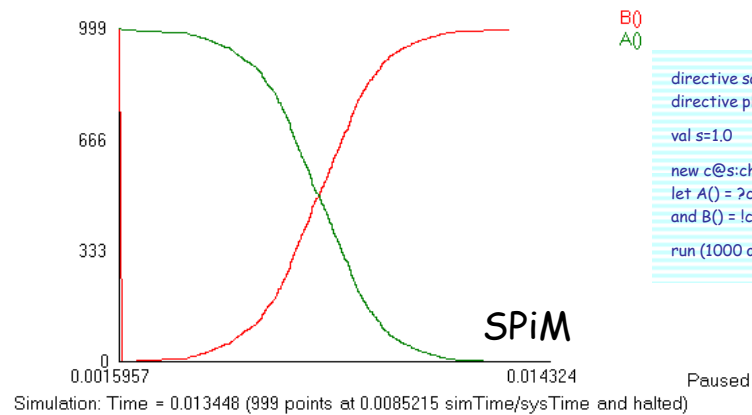
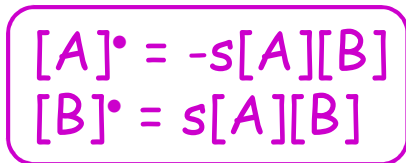
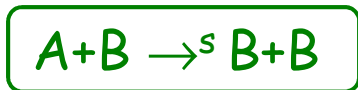
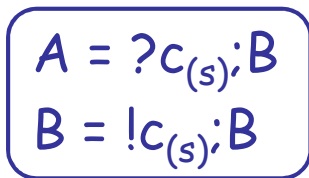
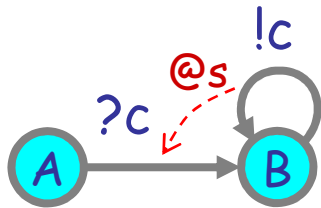
- For each  $E$  there is an  $E' \approx E$  that is detangled ( $E' = \text{Pi}(\text{Ch}(E))$ )
- For each  $E$  in automata form there is an  $E' \approx E$  that is detangled and in automata form ( $E' = \text{Detangle}(E)$ ).

# Exercise: Making Waves

Or: build me a population like this:



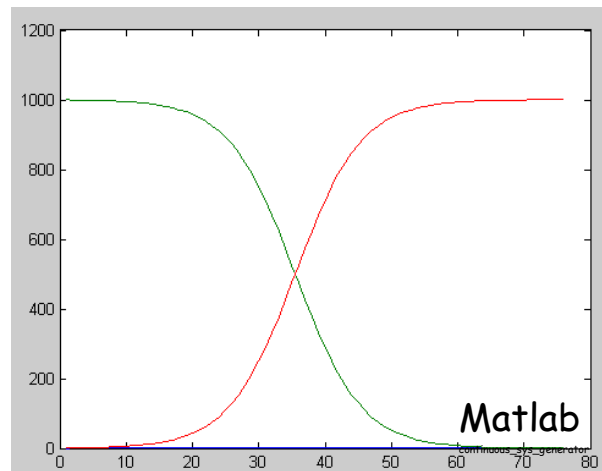
# Nonlinear Transition (NLT)



```

directive sample 0.02 1000
directive plot B(): A()
val s=1.0
new c@s:chan
let A() = ?c; B()
and B() = !c;B()
run (1000 of A() | 1 of B())
    
```

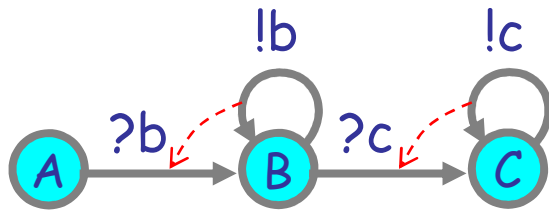
N.B.: needs at least 1 B to "get started".



```

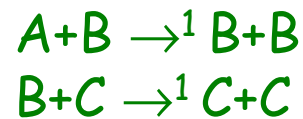
interval/step [0:0.001:0.0]
(A) dx1/dt = - x1*x2    1000.0
(B) dx2/dt = x1*x2     1.0
    
```

# Two NLTs: Bell Shape



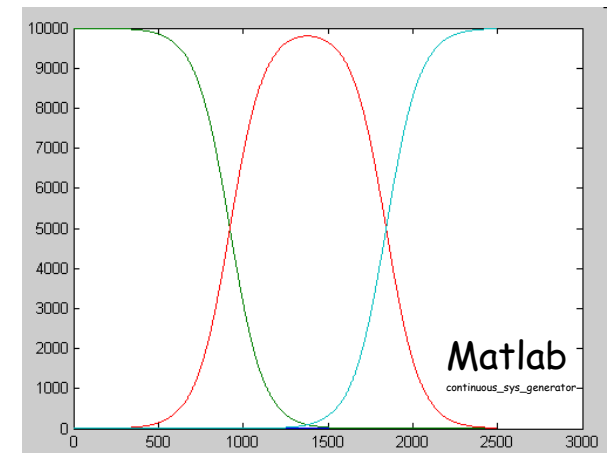
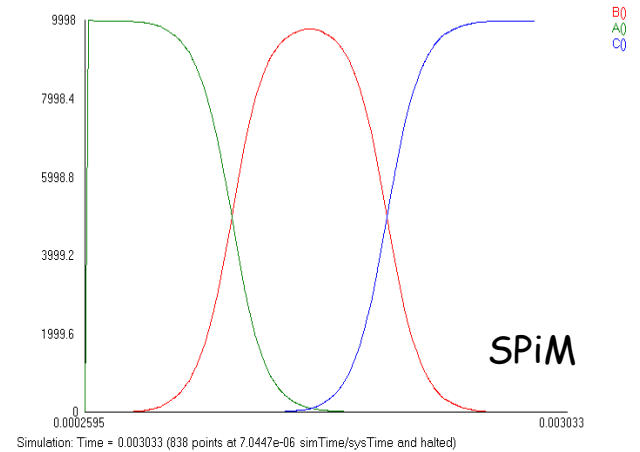
$$[B]^{\bullet} = [B]([A] - [C])$$

$$\begin{aligned} A &= ?b_{(1)}; B \\ B &= !b_{(1)}; B \oplus ?c_{(1)}; C \\ C &= !c_{(1)}; C \end{aligned}$$



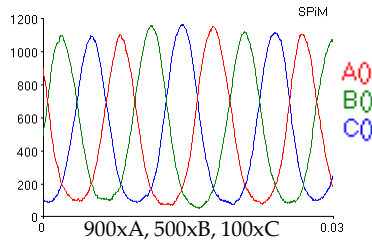
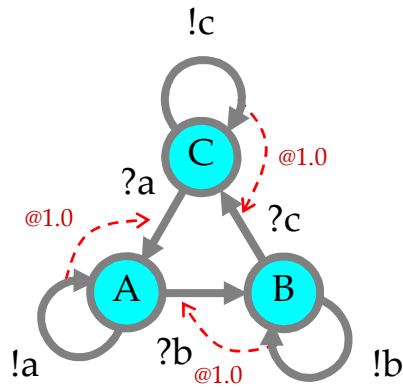
$$\begin{aligned} [A]^{\bullet} &= -[A][B] \\ [B]^{\bullet} &= [A][B] - [B][C] \\ [C]^{\bullet} &= [B][C] \end{aligned}$$

```
directive sample 0.0025 1000
directive plot B(); A(); C()
new b@1.0:chan new c@1.0:chan
let A() = ?b; B()
and B() = do !b;B() or ?c; C()
and C() = !c;C()
run ((10000 of A()) | B() | C())
```



interval/step	[0-0.000001-0.0025]	
(A)	$dx1/dt = -x1*x2$	10000.0
(B)	$dx2/dt = x1*x2 - x2*x3$	1.0
(C)	$dx3/dt = x2*x3$	1.0

# NLT in a Cycle: Oscillator (unstable)



```
directive sample 0.03 1000
directive plot A(): B(): C()
```

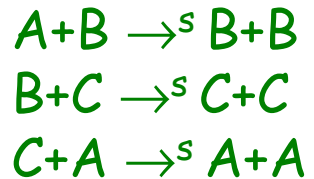
```
new a@1.0:chan new b@1.0:chan new c@1.0:chan
let A() = do !a;A() or ?b; B()
and B() = do !b;B() or ?c; C()
and C() = do !c;C() or ?a; A()
```

```
run (900 of A() | 500 of B() | 100 of C())
```

$$A = !a_{(s)}; A \oplus ?b_{(s)}; B$$

$$B = !b_{(s)}; B \oplus ?c_{(s)}; C$$

$$C = !c_{(s)}; C \oplus ?a_{(s)}; A$$

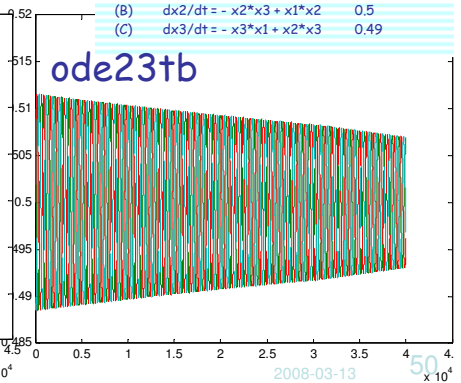
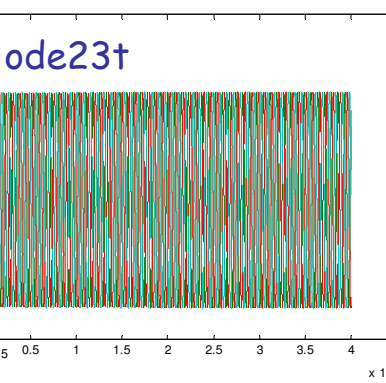
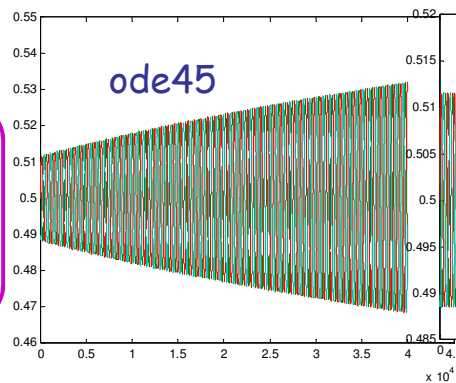
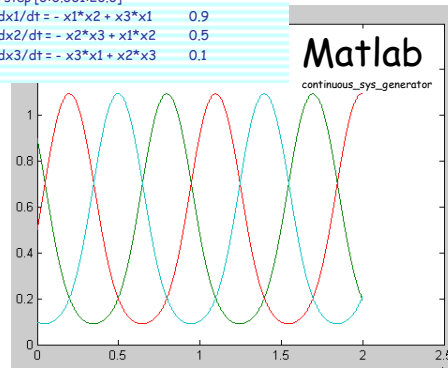


$$[A]^{\bullet} = -s[A][B] + s[C][A]$$

$$[B]^{\bullet} = -s[B][C] + s[A][B]$$

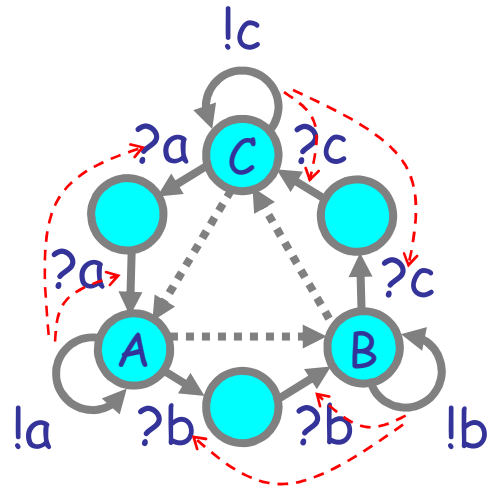
$$[C]^{\bullet} = -s[C][A] + s[B][C]$$

```
interval/step [0:0.001:20.0]
(A) dx1/dt = -x1*x2 + x3*x1 0.9
(B) dx2/dt = -x2*x3 + x1*x2 0.5
(C) dx3/dt = -x3*x1 + x2*x3 0.1
```



```
interval/step [0:0.01:400.0]
(A) dx1/dt = -x1*x2 + x3*x1 0.51
(B) dx2/dt = -x2*x3 + x1*x2 0.5
(C) dx3/dt = -x3*x1 + x2*x3 0.49
```

# Oscillator (stable)



```

directive sample 0.1 1000
directive plot A1(); A2(); A3()

val r=1.0 val s=1.0

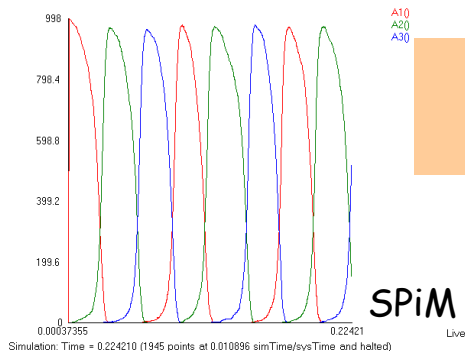
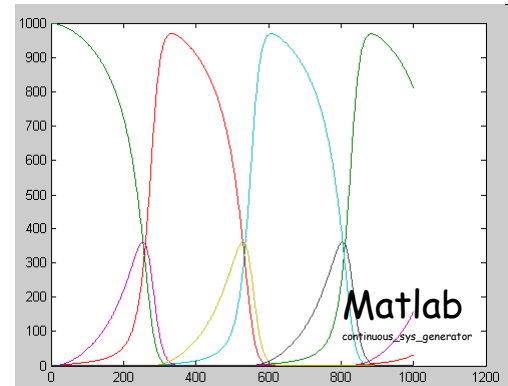
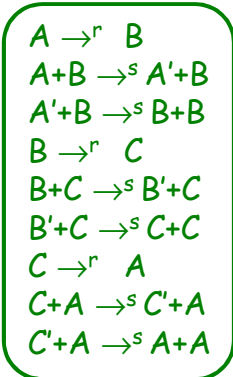
new a1@s:chan new a2@s:chan new a3@s:chan
let A1() = do !a1;A1() or delay@r;A2() or ?a2; ?a2; A2()
and A2() = do !a2;A2() or delay@r;A3() or ?a3; ?a3; A3()
and A3() = do !a3;A3() or delay@r;A1() or ?a1; ?a1; A1()

run 1000 of A1()
    
```

N.B. this does not deadlock!

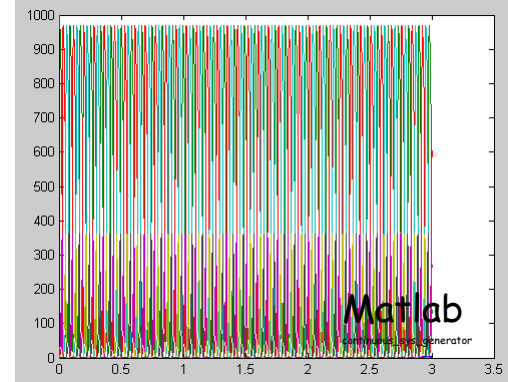
$$\begin{aligned}
 A &= !a_{(s)};A \oplus \tau_r;B \oplus ?b_{(s)};A' \\
 A' &= ?b_{(s)};B \\
 B &= !b_{(s)};B \oplus \tau_r;C \oplus ?c_{(s)};B' \\
 B' &= ?c_{(s)};C \\
 C &= !c_{(s)};C \oplus \tau_r;A \oplus ?a_{(s)};C' \\
 C' &= ?a_{(s)};A
 \end{aligned}$$

Sustained Deterministic Oscillation



Robust Stochastic Oscillation

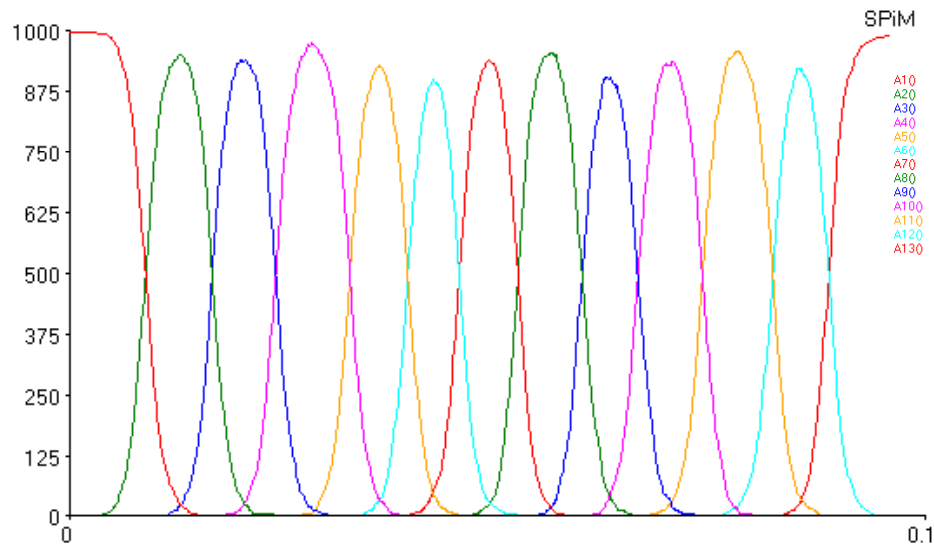
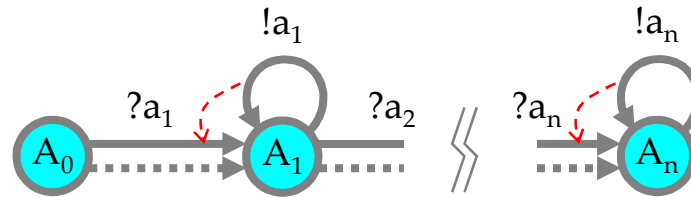
$$\begin{aligned}
 [A]^* &= -r[A] - s[A][B] + r[C] + s[C'][A] \\
 [B]^* &= -r[B] - s[B][C] + r[A] + s[A'][B] \\
 [C]^* &= -r[C] - s[C][A] + r[B] + s[B'][C] \\
 [A']^* &= -s[A'][B] + s[A][B] \\
 [B']^* &= -s[B'][C] + s[B][C] \\
 [C']^* &= -s[C][A] + s[C][A]
 \end{aligned}$$



```

interval/step [0:0.0001:0.1]
(A) dx1/dt = -x1 - x1^2*x2 + x3 + x6^4*x1 1000.0
(B) dx2/dt = -x2 - x2^4*x3 + x1 + x6^4*x2 0.0
(C) dx3/dt = -x3 - x3^4*x1 + x2 + x5^4*x3 0.0
(A') dx4/dt = -x4^4*x2 + x7^4*x2 0.0
(B') dx5/dt = -x5^4*x3 + x2^4*x3 0.0
(C') dx6/dt = -x6^4*x1 + x3^4*x1 0.0
    
```

# NLTs in Series: Soliton Propagation



```
directive sample 0.1 1000
directive plot A1(); A2(); A3(); A4(); A5(); A6(); A7(); A8();
A9(); A10(); A11(); A12(); A13()
```

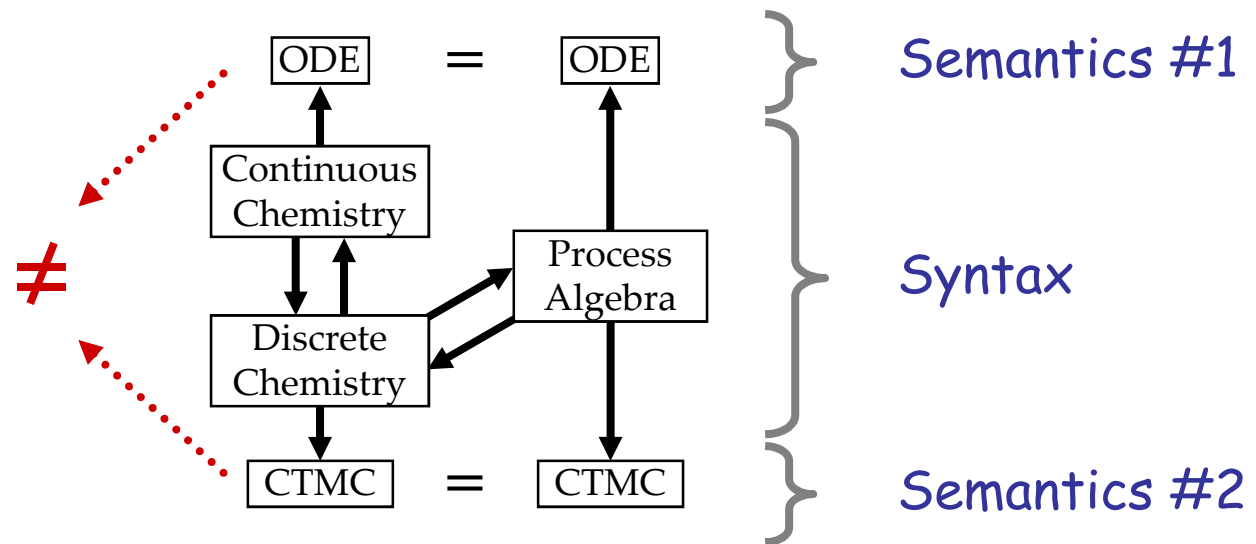
```
val r=1.0 val s=1.0
```

```
new a2@s:chan new a3@s:chan new a4@s:chan
new a5@s:chan new a6@s:chan new a7@s:chan
new a8@s:chan new a9@s:chan new a10@s:chan
new a11@s:chan new a12@s:chan new a13@s:chan
let A1() = do delay@r:A2() or ?a2; A2()
and A2() = do la2;A2() or delay@r:A3() or ?a3; A3()
and A3() = do la3;A3() or delay@r:A4() or ?a4; A4()
and A4() = do la4;A4() or delay@r:A5() or ?a5; A5()
and A5() = do la5;A5() or delay@r:A6() or ?a6; A6()
and A6() = do la6;A6() or delay@r:A7() or ?a7; A7()
and A7() = do la7;A7() or delay@r:A8() or ?a8; A8()
and A8() = do la8;A8() or delay@r:A9() or ?a9; A9()
and A9() = do la9;A9() or delay@r:A10() or ?a10; A10()
and A10() = do la10;A10() or delay@r:A11() or ?a11; A11()
and A11() = do la11;A11() or delay@r:A12() or ?a12; A12()
and A12() = do la12;A12() or delay@r:A13() or ?a13; A13()
and A13() = la13;A13()
```

```
run 1000 of A1()
```



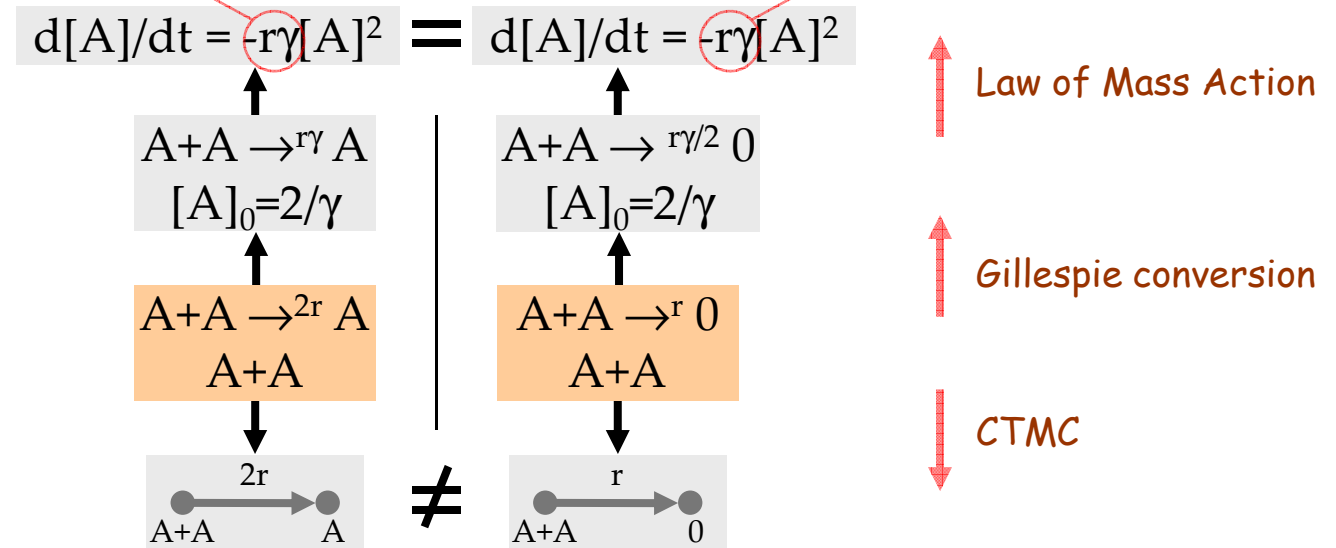
# GMA $\neq$ CME



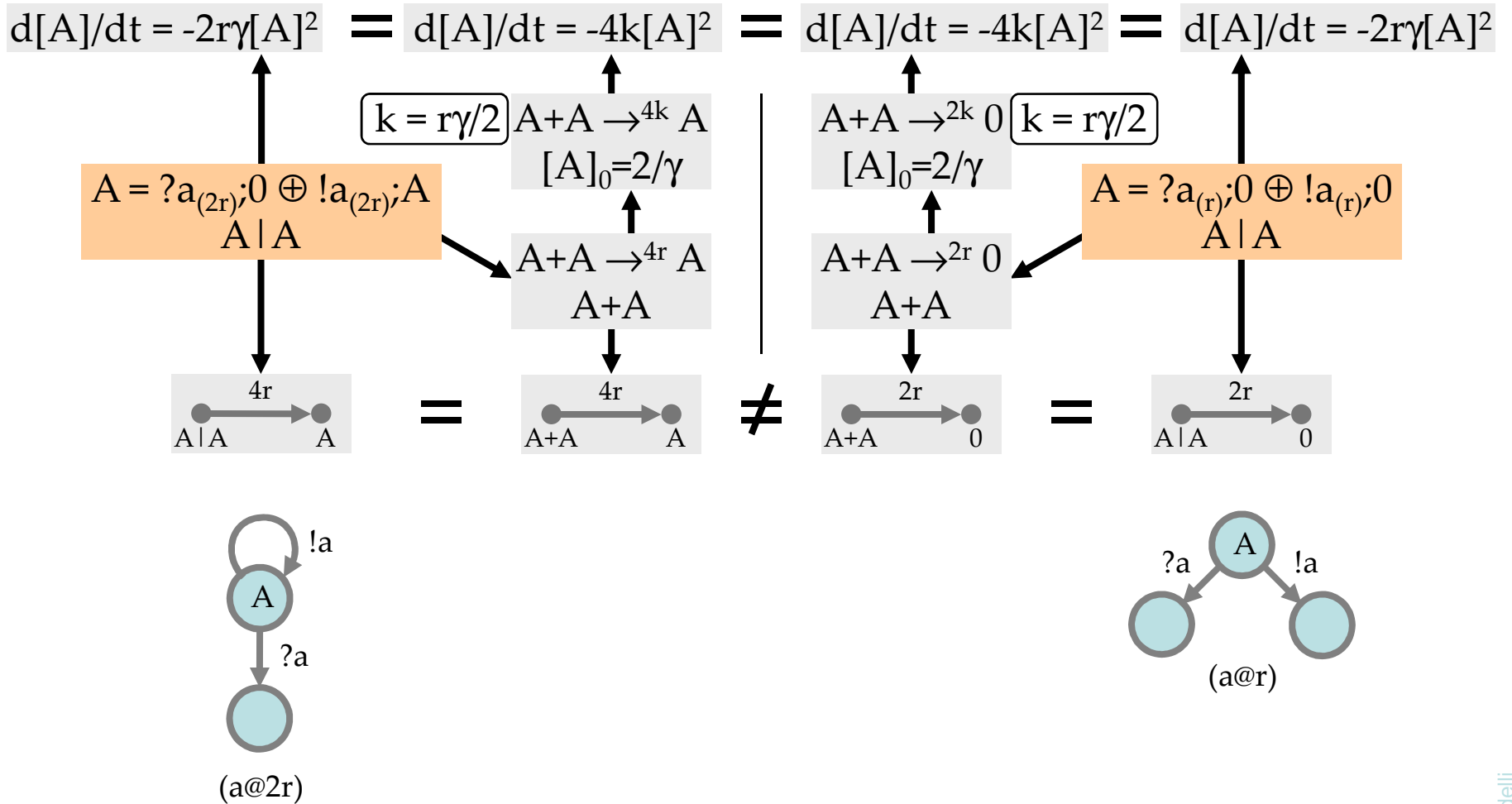


1\*reaction rate  $r\gamma$  because  
1\*A is lost in reaction.

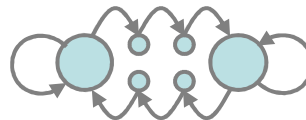
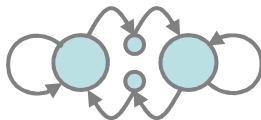
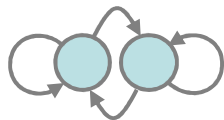
2\*reaction rate  $r\gamma/2$  because  
2\*A are lost in reaction.



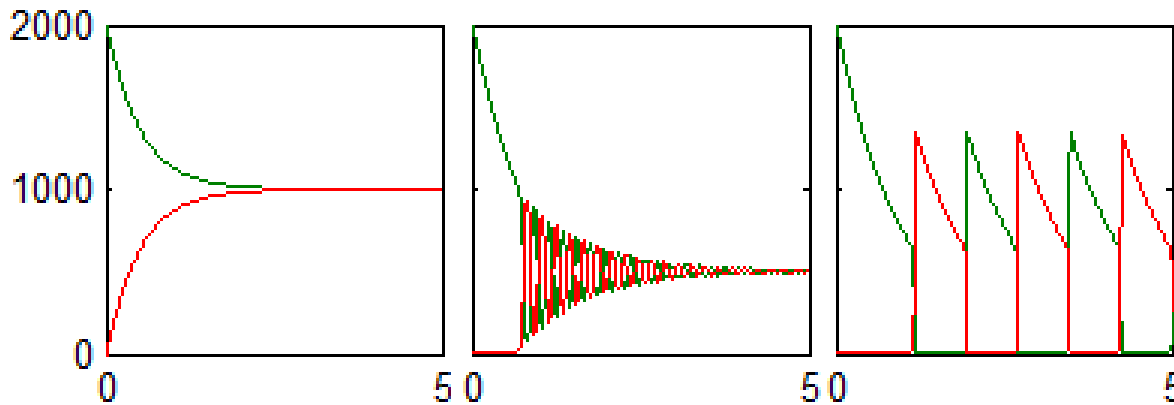
# ... as Automata



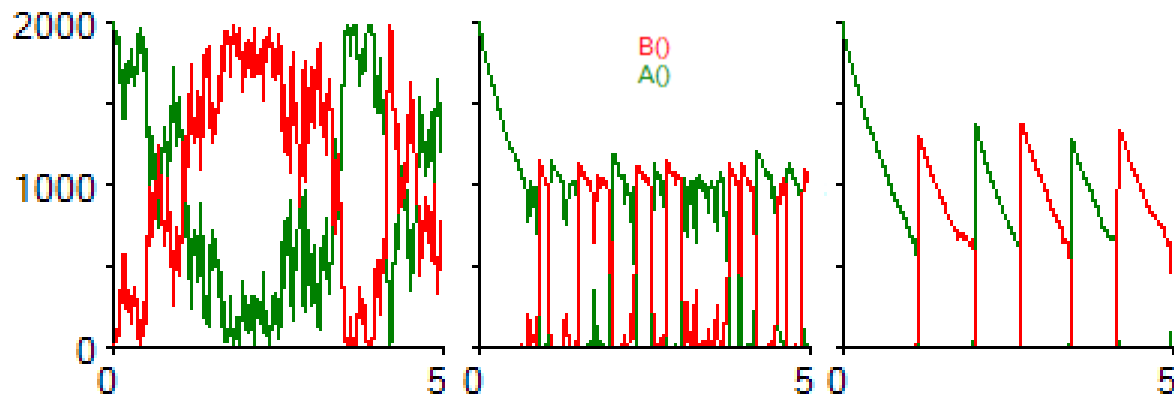
# Continuous vs. Discrete Groupies



(all with doping)



Matlab



SPiM

$2000 \times A, 0 \times B, 1 \times A_d, 1 \times B_d, r = 1.0$

```
directive sample 5.0 1000
directive plot B0; A0
new a@1.0(chan)
new b@1.0(chan)
let A0 = do {a; A0} or {b; B0}
and B0 = do {b; B0} or {a; A0}
let Ad0 = {a; Ad0}
and Bd0 = {b; Bd0}
run 2000 of A0
run 1 of (Ad0 | Bd0)
```

```
directive sample 5.0 1000
directive plot B0; A0
new a@1.0(chan)
new b@1.0(chan)
let A0 = do {a; A0} or {b; B0}
and B0 = do {b; B0} or {a; A0}
let Ad0 = {a; Ad0}
and Bd0 = {b; Bd0}
run 2000 of A0
run 1 of (Ad0 | Bd0)
```

```
directive sample 5.0 1000
directive plot B0; A0
new a@1.0(chan)
new b@1.0(chan)
let A0 = do {a; A0} or {b; B0}
and B0 = do {b; B0} or {a; A0}
let Ad0 = {a; Ad0}
and Bd0 = {b; Bd0}
run 2000 of A0
run 1 of (Ad0 | Bd0)
```

```
Groupes ODEs - Groupies.mat
[0;0;0;5;0] r=1.0 k=1.0
A dx1/dt=x1^4-x3^2-x1-x4, 2000.0
A' dx2/dt=x3^2-x1-x3-x2-x2, 0.0
B dx3/dt=x3^2-x1-x3-x3-x2, 0.0
B' dx4/dt=x1^2-x3-x1^2-x3-x5, 0.0
```

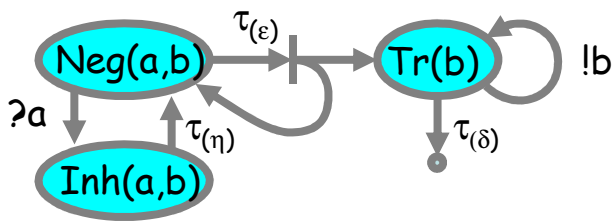
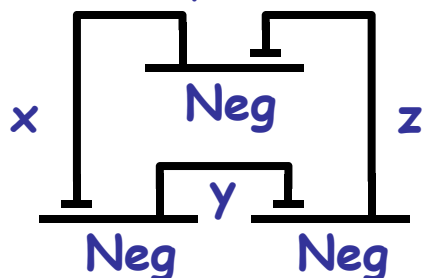
```
Groupes ODEs - Groupies Hysteric 1.mat
[0;0;0;5;0] r=1.0 k=1.0
A dx1/dt=x1^4-x3^2-x1-x4, 2000.0
A' dx2/dt=x3^2-x1-x3-x2-x2, 0.0
B dx3/dt=x3^2-x1-x3-x3-x2, 0.0
B' dx4/dt=x1^2-x3-x1^2-x3-x5, 0.0
```

```
Groupes ODEs - Groupies Hysteric 2.mat
[0;0;0;5;0] r=1.0 k=1.0
A dx1/dt=x1^4-x3^2-x1-x4, 2000.0
A' dx2/dt=x3^2-x1-x3-x2-x2, 0.0
A'' dx5/dt=x3^2-x3-x3^5-x2-x5, 0.0
B dx3/dt=x3^2-x1-x3-x3-x2, 0.0
B' dx4/dt=x1^2-x3-x1^2-x3-x5, 0.0
B'' dx6/dt=x1^2-x3-x3-x5-x6, 0.0
```

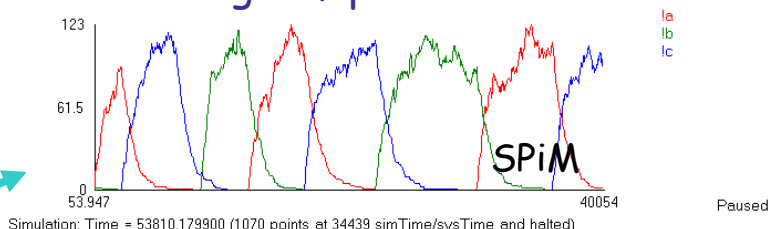
# And Yet It Moves

R.Blossey, L.Cardelli, A.Phillips:  
 Compositionality, Stochasticity and  
 Cooperativity in Dynamic Models of  
 Gene Regulation (HFSP Journal)

## The Repressilator



A fine stochastic oscillator over  
 a wide range of parameters.



## Parametric representation

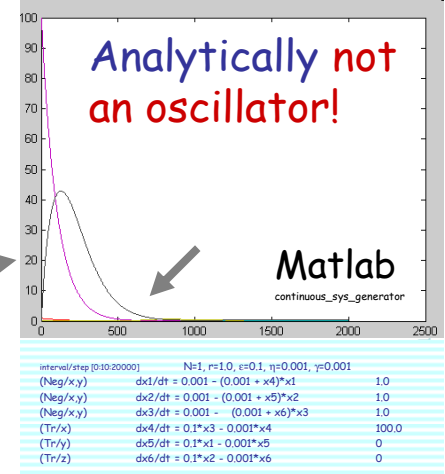
$$\begin{aligned} \text{Neg}(a,b) &= ?a; \text{Inh}(a,b) \oplus \tau_\epsilon; (\text{Tr}(b) \mid \text{Neg}(a,b)) \\ \text{Inh}(a,b) &= \tau_\eta; \text{Neg}(a,b) \\ \text{Tr}(b) &= !b; \text{Tr}(b) \oplus \tau_\delta; 0 \\ \text{Neg}(x_{(r)}, y_{(r)}) &\mid \text{Neg}(y_{(r)}, z_{(r)}) \mid \text{Neg}(z_{(r)}, x_{(r)}) \end{aligned}$$

$$\begin{aligned} d[\text{Neg}/x,y]/dt &= -r[\text{Tr}/x][\text{Neg}/x,y] + \eta[\text{Inh}/x,y] \\ d[\text{Neg}/y,z]/dt &= -r[\text{Tr}/y][\text{Neg}/y,z] + \eta[\text{Inh}/y,z] \\ d[\text{Neg}/z,x]/dt &= -r[\text{Tr}/z][\text{Neg}/z,x] + \eta[\text{Inh}/z,x] \\ d[\text{Inh}/x,y]/dt &= r[\text{Tr}/x][\text{Neg}/x,y] - \eta[\text{Inh}/x,y] \\ d[\text{Inh}/y,z]/dt &= r[\text{Tr}/y][\text{Neg}/y,z] - \eta[\text{Inh}/y,z] \\ d[\text{Inh}/z,x]/dt &= r[\text{Tr}/z][\text{Neg}/z,x] - \eta[\text{Inh}/z,x] \\ d[\text{Tr}/x]/dt &= \epsilon[\text{Neg}/z,x] - \gamma[\text{Tr}/x] \\ d[\text{Tr}/y]/dt &= \epsilon[\text{Neg}/x,y] - \gamma[\text{Tr}/y] \\ d[\text{Tr}/z]/dt &= \epsilon[\text{Neg}/y,z] - \gamma[\text{Tr}/z] \end{aligned}$$

$$\begin{aligned} \text{Neg}/x,y &\xrightarrow{\epsilon} \text{Tr}/y + \text{Neg}/x,y \\ \text{Neg}/y,z &\xrightarrow{\epsilon} \text{Tr}/z + \text{Neg}/y,z \\ \text{Neg}/z,x &\xrightarrow{\epsilon} \text{Tr}/x + \text{Neg}/z,x \\ \text{Tr}/x + \text{Neg}/x,y &\xrightarrow{r} \text{Tr}/x + \text{Inh}/x,y \\ \text{Tr}/y + \text{Neg}/y,z &\xrightarrow{r} \text{Tr}/y + \text{Inh}/y,z \\ \text{Tr}/z + \text{Neg}/z,x &\xrightarrow{r} \text{Tr}/z + \text{Inh}/z,x \\ \text{Inh}/x,y &\xrightarrow{\eta} \text{Neg}/x,y \\ \text{Inh}/y,z &\xrightarrow{\eta} \text{Neg}/y,z \\ \text{Inh}/z,x &\xrightarrow{\eta} \text{Neg}/z,x \\ \text{Tr}/x &\xrightarrow{\gamma} 0 \\ \text{Tr}/y &\xrightarrow{\gamma} 0 \\ \text{Tr}/z &\xrightarrow{\gamma} 0 \\ \text{Neg}/x,y + \text{Neg}/y,z + \text{Neg}/z,x & \end{aligned}$$

simplifying (N is the quantity  
 of each of the 3 gates)

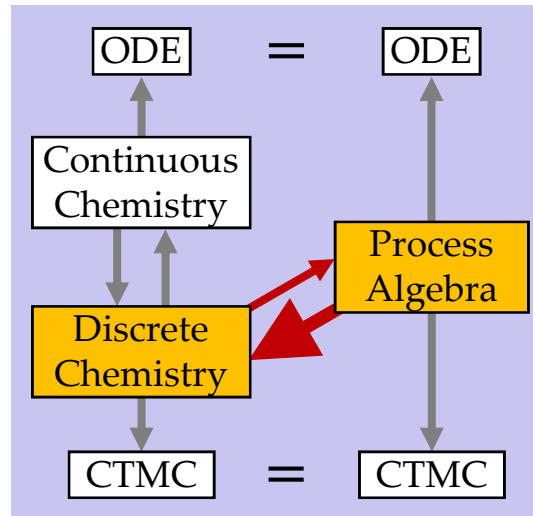
$$\begin{aligned} d[\text{Neg}/x,y]/dt &= \eta N - (\eta + r[\text{Tr}/x])[\text{Neg}/x,y] \\ d[\text{Neg}/y,z]/dt &= \eta N - (\eta + r[\text{Tr}/y])[\text{Neg}/y,z] \\ d[\text{Neg}/z,x]/dt &= \eta N - (\eta + r[\text{Tr}/z])[\text{Neg}/z,x] \\ d[\text{Tr}/x]/dt &= \epsilon[\text{Neg}/z,x] - \gamma[\text{Tr}/x] \\ d[\text{Tr}/y]/dt &= \epsilon[\text{Neg}/x,y] - \gamma[\text{Tr}/y] \\ d[\text{Tr}/z]/dt &= \epsilon[\text{Neg}/y,z] - \gamma[\text{Tr}/z] \end{aligned}$$



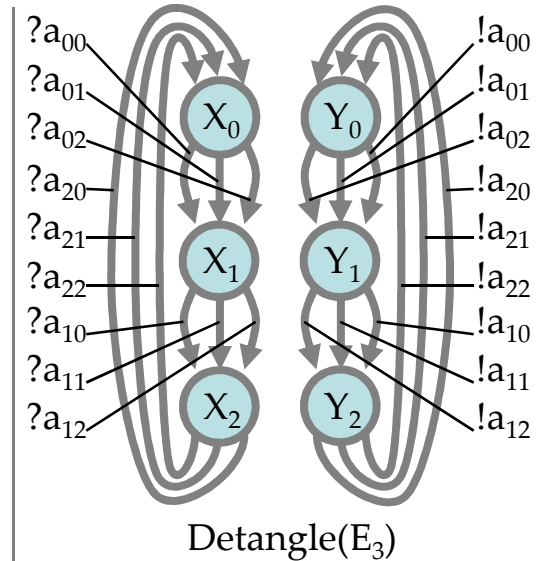
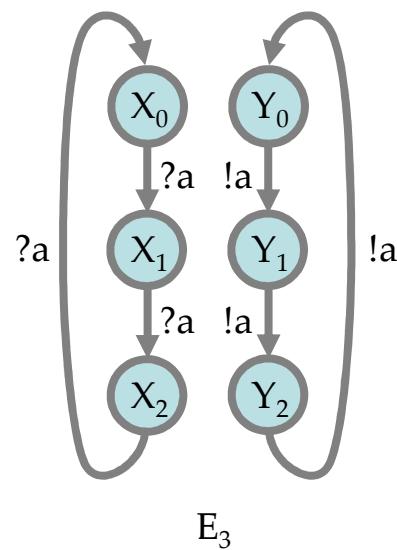
```

internal/step [0-10-20000]  N=1, r=1.0, epsilon=0.1, eta=0.001, gamma=0.001
(Neg/x/y)  dx1/dt = 0.001 - (0.001 + x4)*x1  1.0
(Neg/x/y)  dx2/dt = 0.001 - (0.001 + x5)*x2  1.0
(Neg/x/y)  dx3/dt = 0.001 - (0.001 + x6)*x3  1.0
(Tr/x)     dx4/dt = 0.1*x3 - 0.001*x4  100.0
(Tr/y)     dx5/dt = 0.1*x1 - 0.001*x5  0
(Tr/z)     dx6/dt = 0.1*x2 - 0.001*x6  0
    
```

# Model Compactness



# Entangled vs detangled



(closely related to  $\text{Pi}(\text{Ch}(E_3))$ )

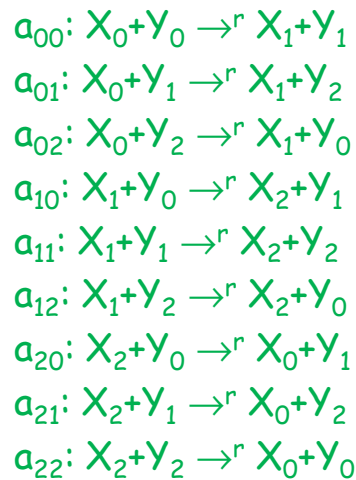
# $n^2$ Scaling Problems

- $E_n$  has  $2n$  variables (nodes) and  $2n$  terms (arcs).
- $Ch(E_n)$  has  $2n$  species and  $n^2$  reactions.
- The stoichiometric matrix has size  $2n \cdot n^2 = 2n^3$ .
- The ODEs have  $2n$  variables and  $2n(n+n) = 4n^2$  terms  
(number of variables times number of accretions plus depletions when sums are distributed)

$E_3$

$$\begin{aligned} X_0 &= ?a_{(r)}:X_1 \\ X_1 &= ?a_{(r)}:X_2 \\ X_2 &= ?a_{(r)}:X_0 \\ Y_0 &= !a_{(r)}:Y_1 \\ Y_1 &= !a_{(r)}:Y_2 \\ Y_2 &= !a_{(r)}:Y_0 \end{aligned}$$

$Ch(E_3)$

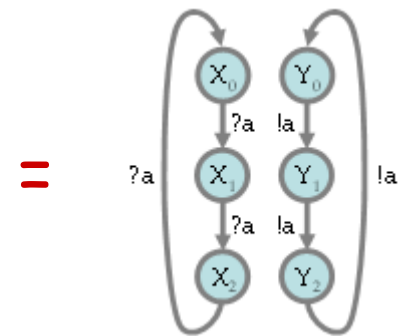


StoichiometricMatrix( $Ch(E_3)$ )

	$a_{00}$	$a_{01}$	$a_{02}$	$a_{10}$	$a_{11}$	$a_{12}$	$a_{20}$	$a_{21}$	$a_{22}$
$X_0$	-1	-1	-1				+1	+1	+1
$X_1$	+1	+1	+1	-1	-1	-1			
$X_2$				+1	+1	+1	-1	-1	-1
$Y_0$	-1		+1	-1		+1	-1		+1
$Y_1$	+1	-1		+1	-1		+1	-1	
$Y_2$		+1	-1		+1	-1		+1	-1

ODE( $E_3$ )

$$\begin{aligned} d[X_0]/dt &= -r[X_0][Y_0] - r[X_0][Y_1] - r[X_0][Y_2] + r[X_2][Y_0] + r[X_2][Y_1] + r[X_2][Y_2] \\ d[X_1]/dt &= -r[X_1][Y_0] - r[X_1][Y_1] - r[X_1][Y_2] + r[X_0][Y_0] + r[X_0][Y_1] + r[X_0][Y_2] \\ d[X_2]/dt &= -r[X_2][Y_0] - r[X_2][Y_1] - r[X_2][Y_2] + r[X_1][Y_0] + r[X_1][Y_1] + r[X_1][Y_2] \\ d[Y_0]/dt &= -r[X_0][Y_0] - r[X_1][Y_0] - r[X_2][Y_0] + r[X_0][Y_2] + r[X_1][Y_2] + r[X_2][Y_2] \\ d[Y_1]/dt &= -r[X_0][Y_1] - r[X_1][Y_1] - r[X_2][Y_1] + r[X_0][Y_0] + r[X_1][Y_0] + r[X_2][Y_0] \\ d[Y_2]/dt &= -r[X_0][Y_2] - r[X_1][Y_2] - r[X_2][Y_2] + r[X_0][Y_1] + r[X_1][Y_1] + r[X_2][Y_1] \end{aligned}$$





# Conclusions

# Conclusions

- **Compositional models**
  - Accurate (at the "appropriate" abstraction level).
  - Manageable (so we can scale them up by composition).
  - Executable (stochastic simulation).
- **Analysis techniques**
  - Mathematical techniques: Markov theory, Chemical Master Equation, and Rate Equation
  - Computing techniques: Abstraction and Refinement, Model Checking, Causality Analysis.
- **Many lines of extensions**
  - Parametric processes for model factorization
  - *Poly*automata for **Bio**-Chemistry: complexation and polymerization
  - Ultimately, rich process-algebra based modeling languages.
- **Quantitative techniques**
  - Important in the "real sciences".